BEST AVAILABLE COPY

ALGC 9924 Homo sari ACCC9812 Homo sari ALGC 9821 Homo sari AC132990 Rattus co

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AL66924 : AB : Thear HIG 18-JAN-2002 Homo sapiens chromosome 6 clone XXbac-2'UJ14, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craujata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo,
                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-JAN-2002) Wellcome Dust Sanger Institute, Bluxton,
Cambridgeshire, CHIO 18A, UK. F.Fall enjiftes:
Aumphery Sanger, ac. ok (16me regiments) c. Subrequest Sanger, ac. ok
On Jan 25, 2002 this sequence version replaced allBaSe0865.
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Location/Qualifiers
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90594 109805; contia -3 39212 kp in leaath
69806 109905; qap ot 1.6 kp
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/db_xrel="taxon:9fbf"
/cbromosome "6"
 AL669924
AC008411
AL669821
AC102990
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109906 136657: cont
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                                                                                       July 5, 2092, 04:44:47 : Search time 2150.68 Seconds (Without alignments) 36:11:936 Million cell updates/sec
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced 9i:7708838.
                                                                                                                                                                                                            Consensus quality: 123959 bases at least 040
Consensus quality: 133398 bases at least 020
Consensus quality: 134736 bases at least 030
Consensus quality: 134736 bases at least 020
Estimated insert size: 135340; agarose-fp estimation
Estimated insert size: 135340; agarose-fp estimation
Chality coverage: 4.95 in 020 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 21 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1262: Gap of unknown length

* 2263 5223: Gap of unknown length

* 5324 5323: Gap of unknown length

* 5324 5529: Contig of 9876 bp in length

* 15200 15299: contig of 9876 bp in length

* 15300 22312: Contig of 7013 bp in length

* 22313 22412: gap of unknown length
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contig of 3002 bp in length
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contig of 4946 bp in length
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/db_xref="taxon:9606"
                                                                                            Web site: http://www.jgi.doe.gov
                                      -----Genome Center
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Homo sapiens chromosome 5 clone CTC-281H14, WORKING DRAFT SEQUENCE,
21 ordered pieces.
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Dob Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
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1 (bases 1 to 137545)
DOE Joint Genome Institute.
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llarity 100.0%; Pred. No. 1.3e-160;
Conservative 0; Mismatches 0;
                                                                                                       7624...41360

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90594...109805
/note-"assembly_fragment:01522
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109906...136657
/note-"assembly_fragment:01742
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a 32671 c 32974 g 37117 t 66
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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AC65#21 144742 bp LNA innear HTG 31-JAN-2902 Homo sapieus chromosome 6 clone XXhac-116Al, *** SEQUENTING IN PROCHESS ***, 4 unordered pieces.
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Cambridaeshire, CBL0 18A, UK. Email conquiries issuage acuk conquiery sanger acuk Clone requests: clonerequest sanger acuk ca Jan 15, 2002 this sequence version replaced gi:18152648.
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* NOTE: This is a "working draft, sequence. It currently * consists of 4 contigs. The true order of the pieces * is not known and their order in this sequence record is

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MIZINGO, B. A. Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albarooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blango, K., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burchl, R., Bryant, N.P., Chang, C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Carren, T.F., Carter, M., Doddit, J., Chavez, D., Chen, G., Corn, R., Coyle, N.D., Dany, T.K., Dany, T.K., David, R., David, R., David, M.L., Davis, C.C., David, R., David, R., Davis, C., David, C., David, C., David, M.L., Davis, C., David, R., David, R., Davis, C., David, R., David, R., Davis, C., David, R., David, R., David, R., David, R., Davis, C., David, C., Davis, C., Davis, C., David, C., Davis, C., Davis, C., Carter, David, C., Carter, C., Capis, C., Carter, C., C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 57802 bases at least Q40
Consensus quality: 64028 bases at least Q30
Consensus quality: 67953 bases at least Q20
Estimated insert size: 35926; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 0.4x in Q20 bases; sum-of-contigs estimation
                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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SUMMARIES

Description	DNA euroding misk/ DNA enryching misk/ Genomic DNA #1 enc
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Best Local Similarity (2010) (4) Fred, No. 2010-14;
Matches 275; Conservative (1) Mustaralys
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AAS09958 standard; DNA: 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the coding sequence of cardiac enhancer mCsx/Nkx2.5 homology domains Al + A2 and intervening sequence. The nucleic acid is useful for specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac
                                                                                                                                               DNA encoding mCsx/Nkx2.5 homology domains A1 + A2, and intervening DNA.
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specific enhancer elements may be used for gene therapy
                                                                                                                                                                     mCsx/Nkx2.5 homology domain; cardiac enhancer; cardiac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 375; DB 22;
100.0%; Pred. No. 9.3e-184;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                               ВР
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                                                                             AAS09960 standard; DNA; 1072
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Best Local Similarity 100.
Matches 375; Conservative
                      361 ctgcacaggcgacgc 375
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                                                                                                                                                                                                                                        WO200151006-A2
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nucleic acid is useful for specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac cell-specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac specific enhancer elements may be used for gene therapy.
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acaggaaacgcggagctatttaaaagaccctatcgattactttatctttcctggaaagct
                                                           241 acaggaaacgcggagctatttaaaagaccctatcgattactttatctttcctggaaagct
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100.0%; Pred. No. 8.9e-184;
ive 0; Mismatches 0;
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Matches 375; Conserv
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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July 5, 2002, 04:45:17 ; Search time 80.62 Seconds (without alignments) 1142.552 Million cell updates/sec
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                                                                                                                                                                              375
1 aggaccecegcaeceteate.....agggtetgcaeaggegaege 375
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// cgn2_6/ptodata/2/ina/5A_cMR.seq:*
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// cgn2_6/ptodata/2/ina/6A_cMR.seq:*
// cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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UM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Description

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Result No. Score Match Length DB

No matches found

Search completed: July 5, 2002, 06:10:55 Job time: 5078 sec

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July 5, 2002, 04:51:53 ; Search time 4488.65 Seconds
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| Caga2_6/ptodata/2/pna/USO6_COMB.seq:*
| Caga2_6/ptodata/2/pna/USO7_COMB.seq:*
| Caga2_6/ptodata/2/pna/USO7_COMB.seq:*
| Caga2_6/ptodata/2/pna/USO81_COMB.seq:*
| Caga2_6/ptodata/2/pna/USO82_COMB.seq:*
| Caga2_6/ptodata/2/pna/USO83_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
/con2_6/ptodata/2/pna/US095D_COMB.seq:*
/con2_6/ptodata/2/pna/US095D_COMB.seq:*
/con2_6/ptodata/2/pna/US095A_COMB.seq:*
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Cgn2_6/prodata/2/pna/US08J_COMB.seq:

CGn2_6/ptodata/2/pna/US09_COMB.seq:

CGn2_6/ptodata/2/pna/US09_COMB.seq:

CGn2_6/ptodata/2/pna/US09_COMB.seq:

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CGn2_6/ptodata/2/pna/US094_COMB.seq:
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Copyriati (c) 1994 - Zene Compagn Lid.
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Maximum DB seq length: 2000060000
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Pred. No. is the number of results predicted by charge to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 1. Applications of the sequence of th nesting ton ALL INMENTS Ê Owery Maten Dengih i H 4.1.2 Score Š.

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PC1-US01-01511-1
RESULT
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/cqn2_6/ptodata/2/pnu/USF00U_CMB.seq:* /cqn2_6/ptodata/2/pnu/USF0U_CMB.seq:* /cqn2_6/ptodata/2/pnu/USF0U_Z_WB.seq:* /cqn2_6/ptodata/2/pnu/USF0U_CMB.seq:* /cqn2_6/ptodatu/2/pnu/USF0U_CMB.seq:*

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RESULT 4
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Score 375; DB 1; I
Pred. No. 2.4e-193;
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Pred. No. 2.4e-193;
; Mismatches 0;
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APPLICANT: Lee, IKe W.
APPLICANT: Launo, Seigo
TITLE OF INVENTION: Cardiac-Cell Specific Enhancer FITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 01948/069002
CURRENT APPLICATION NUMBER: US/09/761,466
CURRENT FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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; GENERAL INFORMATION:
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LENGTH: 375
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US-09-761-466-1
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US-09-761-466-1
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Matches 375,
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Pred. No. 2.5e-193;
Mismatches 0;
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Best Local Similarity 100.
Matches 375; Conservative
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ORGANISM: HOMO
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cardiac-Ceil Specific Enhancer Elements
TITLE OF INVENTION: and Uses Thereof
FITLE OF INVENTION: and Uses Thereof
FITLE OF INVENTION: and Uses Thereof
FITLE REPERENCE: 01948/069402
CURRENT APPLICATION NUMBER: PCT/US01/01511
CURRENT FILLING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 66/176,419
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ IN MOSS: 20
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                          APPLICANT: 17umo, Seigo
1TITE OF INVENTION: Cardiac-Cell Specific Enhancer Elements
1TITE OF INVENTION: and USes Thereof
FILE REFERENCE: 01948/065002
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SOFIWARE: FastSEQ for Windows Version 4.0
                                                                                                                                            US/09/761,466
                                                                                                                                                            CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,419
PRIOR FILING DATE: 2000-01-14
Sequence 3, Application US/09761465 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                        CURRENT APPLICATION NUMBER:
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US-09-761-466-3
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                                        APPLICANT: Lee, Tke W. APPLICANT: IZUMG, Sei
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                                                                                                             Length 7838;
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TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 01948/069002
                                                                                                         100.0%; Score 475; DB 1: 1
100.0%; Pred. No. 2.5e-193;
Jve. 0; Mismatches no.
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/761,466
CURRENT FILLING DATE: 2001-61-16
PRIOR APPLICATION NUMBER: US 60/176,415
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NUMBER OF SEQ 15 NGS: 20
SOFTWARE: FastSBy for Windows Version 4.
: LOCATION: (1)...(7838)
; OTHER INFORMATION: n - A,I,C or G
PCT-US01-01511-4
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| Sequence 4, Application US/5/9761466
| GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or
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; OTHER INFORMATION: Incyte ID No: CpG_991027_B15_masked_fa.Contig29958
US-60-182-316-1254
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                                                                                                                                                                                                                                                                                                                                   Sequence 1254, Application US/60182316
GENERAL INFORMATION:
APPLICANT: CURLIS, Anne L.
APPLICANT: Lagace, Robert E.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
TITLE OF INVENTION: CPG Island Polynucleotides
FILE REFERENCE: PX-0003 P
CURRENT APPLICATION NUMBER: US/60/182,316
CURRENT FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 14,630
SOFTWARE: PERL PROGRAM
SEQ ID NO 1254
LENGTH: 338
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Matches 80; Conservative
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ORGANISM: Homo sapiens
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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July 5, 2002, 05:33:03 ; Search time 248.75 Seconds (without alignments) 2425.605 Million cell updates/sec
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OM nucleic - nucleic search, using sw model
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cqn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq:* Database :

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Result Goorg No. Score Match Length DB ID

Description

No matches found

Search completed: July 5, 2002, 07:36:39 Job time: 7416 sec

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GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.
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July 5, 2002, 04:44:12; Search time 2730.19 Seconds (without alignments) 1853.848 Million cell updates/sec
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Description

Search completed: July 5, 2002, 05:32:51 Job time: 2919 sec

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No matches found

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July 5, 2002, 06:10:09 : Search time 2160.68 Seconds (without alianments) 454.943 Million cell appares/sec
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Submitted (77-ANN-2002) Well-come frust Sammer Institute, Hinzton, cambridgeshire, CHO 18A, UK. F-mail et publissi
Mungapryssamer, acid (2000 requests concrement sammer, acid may 25, 2002 this septence retsion replaced uniB250865.
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Quality coverage: 4.95 in Q20 bases; agarose-fp estimation Quality coverage: 4.91 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft' sequence. It currently consists of 21 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced
* by the finished sequence will be preserved.
* This sequence will be preserved.
* 1 2162: contig of 2162 bp in length
* 2263 5222: contig of 2961 bp in length
* 5224 5323: contig of 9961 bp in length
* 15200 15299: gap of unknown length
* 15200 15299: gap of unknown length
* 15200 22312: contig of 97701 bp in length
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gap of unknown length
contig of 6656 bp in length
gap of unknown length
contig of 3002 bp in length
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/clone_lib="CalTech human BAC library C"
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g of 3002 bp in length
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contig of 9546 bp in length
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of 4336 bp in length
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
Direct Submission
Submitsed (03-40G-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced 91:7708838.
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DOE Joint Genome Institute.
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Consensus quality: 133398 bases at least 030
Consensus quality: 134736 bases at least 020
Estimated insert size: 135340; agarose-fp estimation
Estimated insert size: 13595; sum-of-contigs estimation
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Center: Joint Genome Institute
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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Gaps

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AL669821 144702 bp DNA linear HTG 31-JAN-2002
Homo sapiens chromosome 6 clone XXbac-116A1, *** SEQUENCING IN
PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                       Pashingston Direct Submission Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries:

UmunquerySanger.ac.uk Clone requests: clonerequest3sanger.ac.uk
On Jan 15, 2002 this sequence version replaced qi:18152648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGA44, version 4.5
Sequencing vector: plasmid: 108752; 100% of reads
Chemistry: DW-terminator Big Dye; 100% of reads
Consensus quality: 144176 bases at least 040
Consensus quality: 14423 bases at least 030
Consensus quality: 14429 bases at least 030
Consensus quality: 14429 bases at least 020
Lisert size: 144402; sum-of-contigs
Consensus quality: 1428 error: aquarose-fp
Consensus quality: 1000 bases; agarose-fp
Coverage: 10.72x in 020 bases; sum-of-contigs quality
                                                                                                                              AL669821.4 GI:18157151
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sives of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75529 76028: gap of 100 bp 76029 116346: cont.iq of 40318 bp in length 116447 115446: gap of 100 bp 100 bp 115447 115158: cont.iq of 14812 bp in length 13.259 144702: cont.iq of 13344 bp in length.
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/note="assembly_fragment:03493
fragment_chain:1"
116447. .1910f.
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humguery?sanger.ac.uk
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/chromosome="6"
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/clone_lib="CHCRI-501"
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Mashreghi-Mohammadi,M.
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clone_end:SP6

Search completed: July 5, 2002, 06:10:19 Job time: 5132 sec

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AAS09959 standard; DNA; 5; RP.

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Genrore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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nucleic search, using sw mode.

Puly 5, 2002, (6:17:20 : Search time 341.99 Seconds (without alignments) 256.99 Million geli updates/sec Puri on:

US-09-761-466-2 51

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Post-processing: Listing first 4° summaries

Database :

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| S1DS1/gcadata/roid-genesely/genesegn-emb] (NA1995, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb] (NA1995, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb] (NA1997, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb] (NA1999, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA1999, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA1999, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA21999, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA21999, DA11878)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA2001A.1NA188)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA2001A.1NA188)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA2001A.1NA188)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA2001A.1NA188)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA2001A.1NA188)| S1DS1/gcadata/roid-genesely/genesegn-emb| (NA2001A.1NA1888)| S1DS1/gcadata/roid-genesely/genesegn-emb| SNA2001A.1NA1888| S1DS1/gcadata/roid-genesely/genesegn-emb| SNA2001A.1NA1888| SDS1/gcadata/roid-genesely/genesegn-emb| SNA2001A.1NA1888| SDS1/gcadat

/SIDS1/gradata/rold-geneseq/genesegn-emb1/NA2002.DAI:*

Fred. No. is the number of resolts predicted by chance to have a score areater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ENA encoding mCsx/ ENA encoding mCsx/ Genomic ENA #1 enc Desgription 22 AAS 3959 22 AAS 39560 22 AAS 39961 Score Match Length DB 91 1572 7636 Ř.

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Therapoutie; heart tissue; done therapy; mouse, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mcsx/Mkx2.5 homology domains A1 + A2 and intervening sequence. The nucleic acid is useful for specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac cell-specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac specific enhancer elements may be used for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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therapeutic; heart tissue; gene therapy; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents the coding sequence of cardiac enhancer
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                                                                                                                                               (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
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                                              16-JAN-2001; 2001WO-US01511.
                                                                                              14-JAN-2000; 2000US-0176419
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19-JUL-2001
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                         nucleic acid is useful for specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac cell-specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac specific enhancer elements may be used for gene therapy.
The sequence represents the genomic sequence #1 of human Csx/Nkx2.5. The
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                 Sequence 7836 BP; 2164 A; 1938 C; 1907 G; 1825 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tgctccttttaagggcttgaatgtctgcaactgtcatgtgtacacttaaag
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 22;
100.0%; Pred. No. 2.6e-19;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.0
Matches 51, Conservative
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5, 2002, 06:17:00 Search completed: July Job time: 5398 sec

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September version 4.5 Capyright (c) 1994 - 2060 Compuser Ltd.
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A nucleic - nuclêic search, using sw model

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July 5, 2002, 06:10:55 : Scarch time 80.62 Seconds (without alignments) 155,887 Million cell spares/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fred. No. is the number of results predicted by chance to have a score areater than or equal to the score \beta the result being primited and is derived by analysis of the total score distribution.
                                                                         US-09-761-466-2
51
1 igctccttttaagyqcttga......tgtcatqtqtaracttaaag 51
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Search completed: July 5, 2002, 06:10:55 Job time: 5078 sec

SUMMAFIES

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July 5, 2082, 65:32:51; Search time 2730.19 Seconds (without alignments) 252.123 Million cell updates/sec
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51
I Geteettitaaqugelida.....tglealgigiacaettaaaq 51
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Capyright (c) 1993 - 2000 Campugen Ltd.
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Description:

Search completed: 342y 5, 2002, 05:32:51 Job time: 2919 sec

SUMMAFIES

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Res : 1: No.

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Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 134624 bases at least 040
Consensus quality: 135712 bases at least 030
Consensus quality: 135772 bases at least 020
Insert size: 136057; sum-of-contigs
Insert size: 115180; 6.1% error; agarose-fp
Quality coverage: 7.81x in 020 bases; sum-of-contigs Quality
coverage: 9.23x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* aris not known and their order in this sequence record is
* arbitrary Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41461 47515: contig of 6055 pp in length 47516 47615; gap of 100 bp 100 bp 47516 47615; gap of 100 bp 52830 52929; gap of 100 bp 52830 90493: contig of 37564 bp in length 90494 90593: gap of 100 bp 100 bp 100806 109805: contig of 19212 bp in length 109806 109805; gap of 100 bp 100 bp 100906 136657: contig of 26752 bp in length.
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7624 41360: contig of 33737 bp in length
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                                                                                                      Assembly program: XGAP4; version 4.5
                           --- Project Information
                                                                                Summary Statistics
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/db_xref="taxon:9606"
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/clone_lib="CHORI-501"
humquery@sanger.ac.uk
                                                    Center project name: bPG250J14
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AL669821 144702 bp DNA linear HTG 31-JAN-2002 Homo sapiens chromosome 6 clone XXbac-116A1, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                           54108
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                                          agggggggggggcccaagccgagggcgctgcgcctgaccccgagcggaagggccccagt
                                                                                     ctaggtcctaatgcgggtggcgtctcctttgacaggcggcgtttggggacaacagcgggg
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                                                                                                                                                                                                                                                              ggtctgcacaggcgacgcacaattcggcgcggggaaagcaaaaacacactgacgcttaga
                                                                                                                                                                                                                                                                                                        gtgcacaaacgtgtgtgttcccagagcagctccagagtgcggcagggacgctgggggcgg
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AL669821.4 GI:18157151
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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AL669821
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Gaps

3;

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Conservative

al Similarity 907; Conserv

Best Local Matches 90

Query Match

Length 136657

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DB

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62.2%; Score 667; 99.7%; Pred. No. 0;

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ACU08412 TYP54F bg TAA Threat HTG FP-HTL-2"QU
HOMO Sapiens chromosome 5 clone CIC-2BHHA, WHKHNG DRAFI SEUBENTE.
21 ordered pieces.
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8430 GIGGACAAACGIGIGIGITYYCAGAGAGAI SYASAGIGYYSYAGGAGGIGGGGGGG
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                                         Homo sapiens
Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                   Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humqvery?sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk
On Jan 15, 2002 this sequence version replaced q1:18152648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 144402; sum-of-contigs
Insert size: 167909; 14.3% error; aqarose-fp
Quality coverage: 10.72% in Q20 bases; sum-of-contigs Quality
coverage: 9.55% in Q20 bases: aqarose-tp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently rousists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery*sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
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DOE Joint Genome Institute.
DISTRICT Submitssion
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7708838.
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 137545)
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g of 3002 bp in length
f unknown length
g of 2412 bp in length
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of 7271 bp in 1
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Center Project Name: 293265
Center clone name: CIT-HSPC_281H14
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                                                                                      Sequencing of Human Chromosome
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Center: Joint Genome Institute
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AUTHORS
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JOURNAL
                                                                  REFERENCE
                  KEYWORDS
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                               128198: contig of 9546 bp in length 128298: gap of unknown length 130123: contig of 1825 bp in length 130223: gap of unknown length 134038: contig of 3815 bp in length 134138: gap of unknown length 136470: contig of 2332 bp in length 136570: gap of unknown length 135570: gap of unknown length
                                                                                                                                                                                                                                                                        /clone="CTC-281H14"
/clone_lib="CalTech human BAC library C"
32308 c 31466 g 34494 t 2000 others
bp in length
                   length
   3307
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/db_xref="taxon:9606"
/chromosome="5"
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   contig
gap of
                 118652:
128198:
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Best Local Similarity 99.6
Matches 906; Conservative
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ALL36219 167830 kp DNA linear PkI 05-JAN-2031
Humas DNA sequence from clone PPII-14987 on chromosome 75, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as follows. An attempt is made to resolve all Sequencina problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' restare key.
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Furing sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations to expediter with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutoleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Home.
1 (bases 1 to 167830)
Wall.M.
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Emi, EMBL, Sw., SWISSPROT: Ir., TREMHL, Wp., WORMPEP, Information
on the WORMPEP database can be found at
                             29151 GCCAACATGSTGAAACCTGTGCAAAAAAAAATTAGCGGGGATGGTGATG 2920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
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lett end of clone RP11-110KB is at 155804 in this sequence. The
true right end of clone RP11-453M3 is at 117835 in this sequence.
                                                                                                                                                                                                                                                                   2-221 - 31GCC1G1GATCCCAGCIACTCGGAGCTGAGGAGGCAGGAGAATCGCTTGAACCAGAAA 29280
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CBIÙ ISA, UK. E-mail enquiries: humquery sanger.ac.uk Cloné
                                                                                                                   778 introctal datecengetacted duaque haaggead dadad entigaacendada 1.837
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/db_xref="taxon:1606"
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Britten, M., Editon, L., Nisdanovic, Lordovich, Abroham, R., Allen, N., Gardenson, S., Baldwin, C., Bandan, N., Perker, yie. P., Pedarich, C., Castion, Choepel, Y., Golatorio, M., Perker, yie. P., Pedarich, A., Choepel, Y., Golatorio, M., Perker, S., F. Hymoro, A., Cooke, F., Levin, Landon, K., Heman, R., Domin, M., Perker, D., Cooke, F., Levin, C., Landon, S., Grant, G., Hauds, R., Beatond, A., Horton, C., Adaman, J., Gardin, C., Cartin, C., Levin, R., Beatond, A., Horton, C., London, R., Levin, P., Hort, L., Karatas, A., Klein, J., Landon, S.T., Levin, E., Hort, H., Landon, S., Marchall, M., Medilin, J., Medilin, J., Medilin, J., Marchall, M., Medilin, M., Medilin, M., Medilin, M., Medilin, J., Marchall, M., Medilin, M., Medilin
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Stojanovic, N., Subramanian, A., Tajanas, E., Testaye, S., Theodore, E.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wo, X., Wyman, D., Ye, W.J.,
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Mammalia, Eutherlai Primatesi Tarinibidi, Haminidae, Bomo,
1. (bases i to 1745/2)
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http://itp.genome.washind.ca.com/PM/kep.arMasker.html
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Firect submission
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NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.966731 Consensus quality: 165728 bases at least Q40 Consensus quality: 16751 bases at least Q30 Consensus quality: 171461 bases at least Q20 Insert size: 170000; agarose-fp Quality coverage: 4.5 in Q20 bases; agarose-fp Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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1485 1584: gap of 100 bp
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/clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18942)

1 (bases 1 to 18942)

1 (bases 1 to 18942)

2 Hattori,M., Ishii,K., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 189,492 genomic DNA of 11q23

L Ubblished Only in Database (1999) In press

2 (bases 1 to 189492)

2 (bases 1 to 189492)

3 (bases 1 to 189492)

4 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

5 (bases 1 to 189492)

6 Hattori,M., Tohoki,Y., Watanabe,H. and Sakaki,Y.

7 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

8 Hattori,M., Totoki,Y., Watanabe,H. and Sakaki,Y.

8 Hattori,M., Totoki,Y., Watanabe,H. and Sakaki,Y.

9 Lail: Alabarach (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.go.jp., URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-465-503-9170)

On Nov 22, 2000 this sequence version replaced gi:8119019.
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Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Assembly: Dye-terminator ET-amersham; 100% of reads
Consensus quality: 184605 bases at least Q40
Consensus quality: 186253 bases at least Q30
Consensus quality: 187002 bases at least Q20
Insert size: 187692; sum-of-contigs
Quality coverage: 8.38x in Q20 bases; sum-of-contigs
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Pred. No. 1.2e-45;
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Center code: RIKEN
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/note="assembly_fragment"
eature 81235. .105677
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ieature 105778. .135680
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eature 135781. .174537
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Homo sapiens DNA, clone:RP11-709J7.
Homo sapiens
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Best Local Similarity 100.0
Matches 98; Conservative
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       CONTING ARE TERESONED AS THES N. But the exact sizes of the daps are inknown. This record will be applied with the finished sequence as soon as it is available and the areasson number will be
                                                                                                                                                                                                                                                   #$551 56409 contiq of 4549) bp in length 5551 56409 contiq of 20819 bp in length 57346 88610 contiq of 20819 bp in length 77346 88610 contiq of 12076 bp in length 77346 88610 contiq of 11275 bp in length 119185 119684 contiq of 11275 bp in length 114335 127661 contiq of 4727 bp in length 115375 12765 contiq of 4728 bp in length 116079 152076 contiq of 5938 bp in length 116079 152076 contiq of 6832 bp in length 152177 155008 contiq of 6832 bp in length 152177 155008 contiq of 6832 bp in length 15439 17538 contiq of 6539 bp in length 15439 17538 contiq of 5539 bp in length 15439 17538 contiq of 5539 bp in length 15439 175562 contiq of 5439 bp in length 15439 175562 contiq of 5439 bp in length 18408 18330 contiq of 7549 bp in length 18408 18330 contiq of 7549 bp in length 18408 18502 contiq of 1788 bp in length 18408 185026 contiq of 1788 bp in length 18408 185030 contiq of 1788 bp in length 186026 contid of 1788 bp in length 186026
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152077 152176: qap of 100 bp
152177 159008: contig of 6832 bp in length
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1774 171331: contia of 95
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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Published Only in DataBase (2000) In press
2 (bases 1 to 211344)
Hattori,M., Tshii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Hujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (O2-JUN-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
On Mar 16, 2001 this sequence version replaced gi:11559295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC016765 181047 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 11 clone RP11-555F1, WORKING DRAFT SEQUENCE, 20 unordered pieces.
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Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
On Mar 13, 2000 this sequence version replaced gi:6524271.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 181047)
Waterston, R.H.
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Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 171727 bases at least Q40
Consensus quality: 171727 bases at least Q30
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Center project name: H_NH055F01
Center project name: H_SECTION
Sequencing vector: M13; 81%
Sequencing vector: plasmid; 19%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 68190 AGTGAGCCGAGATCACACCACTGCACCTGGGC 68227
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                                                                                                                                                                                                                               1. .211344
/organism="Homo sapiens"
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/chromosome="11"
                                                                                                                                                                                                                                                                                                      /map="11q"
/clone="RP11-801G16"
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Waterston, R.H.
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AC016765.2 GI:7232204
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AC016765/c
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AUTHORS
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently a consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
Consensus quality: 174384 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 179147; sum-of-contigs
Quality coverage: 3.63 in Q20 bases; sum-of-contigs
Quality coverage: 3.93 in Q20 bases; sum-of-contigs
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10137: gap of unknown length
                                                                                                                                                                                                                                                                               1833: contig of 1833 bp in length
1933: gap of unknown length
3870: contig of 1937 bp in length
3970: gap of unknown length
6886: contig of 2916 bp in length
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gap of unknown length
contig of 5825 bp in length
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contig of 4717 bp in length
gap of unknown length
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gap of unknown length
contig of 8041 bp in length
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contig of 6165 bp in length
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contig of 3066 bp in length
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of 6670 bp in length
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contig of 8772 bp in length
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/note="assembly_name:Contig14"

    1833
/note="assembly_name:Contig13"

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14284. 17263
/note="assembly_name:Contigl8"
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10153. .14183
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/note="assembly_name:Contig15
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/db_xref="taxon:9606"
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ACHORGO Sapiens chromosome 2 clone RP11-1445i, WORKING DRAFI SEQUENCE, 3 unordered pieces.

SCOTENCE, 3 unordered pieces.

ACHORGOZ ACCOGNET OI:14916187

HTG: HTGS_PHASEI; HTGS_DRAFI.
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Pokaryota Matazoa: Choriata: Graniata: Vortebrata: Estrinostomi:
Mammolia: Estbaria: Primates: Jatarrichi: Hominidae: Hom
I (kases 1 to 166434)
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University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an Juli 19, 2001 this sequence gersion replaced gitl01.887 .
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Center code: WUGSC
Web. site:http://genome.wustl.edu/usc/index.shtml
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/note="assembly_name.contiqu"
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Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 175694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 3, 2002 this sequence version replaced 9i:17647080.
                                                                                                                                                                                                                                                                                                                     Louis,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA ( bases 1 to 175694) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
                                                                                                                                                                Isak,A., Kozlowicz,A. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-513019
Unpublished (2002)
3 (base 1 to 175694)
Waterston,R.H.
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_NH0513019
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson. Department of Genetics, Washington University, St. Louis Mo. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-II human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NNIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPII-717A5; the clone sequenced to the left is Actual start of this clone is at base position 1 of RPII-513019; actual end is at base position 904 of RPII-4391.14.

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2625. 2783
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2634. 2783
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/note="match to EST A1971838 (NID:95768664) wv29a02.xl"
4930. .4961
Data from AC096715 was used to finish this clone, AC016753. Location/Qualifiers
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2753. .3323
/NOTE="similar to Homo sapiens EST BG912620
(NID:g14293096)"
3298. .3599
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6241. .6489
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/chromosome="2"
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'/rpt_family="(CACCC)n"

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/note="similar to Sus 1466. .1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anote "match to EST 816.8789 (NIE:q15496729)"
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100.0%; Fred. No. 2.4e-40;
Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77564 CACTGAGRCGAGRCACACTGACLC 77546
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8876. .8935
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10385. .10515
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8649. .8692
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9311. .9448
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w9z1. .11209
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8852. .8672
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8459. .8471
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9464. .9764
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1+732. .10744
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7210. .7290
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7291, .7585
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7586. .7663
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7674. .7938
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7699, 7927
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8422. .8648
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11209. .i1280
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10185, .10223
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/rpt_tamily-"L:"
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129282 149602: contig of 20321 bp in length 149603 149702: gap of 100 bp 149703 178508: contig of 28806 bp in length. Location/Qualifiers
       27387: gap of 100 bp
33448: contig of 6061 bp in length
33548: gap of 100 bp
39008: contig of 5460 bp in length
                                                          39108: gap of 100 bp
44224: contig of 5116 bp in length
44324: gap of 100 bp
50232: contig of 5908 bp in length
                                                                                                              32: gap of 100 bp 58422: contig of 8090 bp in length
                                                                                                                                     58522: gap of 100 bp
64440: contig of 5918 bp in length
27287: contig of 3514 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
1. .1348
/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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39109. .44224
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/db_xref="taxon:9606"
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ACU10984 191540 bp DNA linear PRI 09-JAN-2002 Homo sapiens BAC clone RP11-510C1 from 2, complete sequence. ACU10984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-589-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
4 (bases 1 to 191540)
Waterston, R.H.
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
5 (bases 1 to 191540)
Waterston, R. Borner, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
5 (bases 1 to 191540)
Waterston, R.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
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8.3%; Score 89; DB 2; Length 178508;
Best Local Similarity 100.0%; Pred. No. 2.4e-40;
Matches 89; Conservative 0; Mismatches 0; Indels 0
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The sequence of Homo sapiens BAC clone RP11-510C1
Unpublished (2001)
3 (bases 1 to 191540)
Waterston,R.H.
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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91478. .102460
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102561. .117037
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117138. .129181
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6129. Aare
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6482. .6170
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4724. 4822
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(NID:99810747)"
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7029, 17469
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4298, _3f]6
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(NID:aleM4974:)"
7573. .7812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The clone sequenced to the left is RPIL-397817, 2000 bp overlap; the clone sequenced to the right is A5023040. Actual start of this clone is at base position 29090 of RPII-109612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_tamily="AT_rich"
1426. . 206
/note-"similar to Sus serota ESI BIIB554b (Niligi445947)"
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                                                                                                                                                     OTICE: This sequence may not represent the entire insert of this lone. If may be shorter because we only sequence overlapping fone sections once, of longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                              This sequence was finished as tollows unless otherwise intedi-
a.i rectoms were double straneou, sequenced with an alternate
chemistry. The revered by high publity data (i.e., phied publity ...
39): an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all redions were covered by sequence
trom more than one subclone; and the assembly was continued by
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1449. .1391
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761. .1010
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Contact: sapiens!watson.wastl.odu
                                                                                                                                                                                                                                                       between neighboring data submissions.
                                                       Center project name: H_NH0510031
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/db_xref="taxon:9606"
/cbromosome="2"
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VEClok: pBACe3.6
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55. .455
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Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome Search, 320 Charles Street, Cambridge, MA 02141, USA On Sep 20, 2000 this sequence version replaced gi:7188875.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151865)
                                                                                                      86j9. .865j
/note="match to EST AA704040 (NID:g2713958) ag81f10.rl"
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2.4e-40;
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100.0%; Pred. No. ...
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/rpt_family="(T)n"
8420. .8735
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                                                                                /rpt_family="Alu"
8619. .RFF
                                 /rpt_family="L1"
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9099, 9182
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                              Consequency quality: 146689 bases at 1east 040 consensus quality: 146689 bases at least 030 consensus quality: 149124 bases at least 030 consensus quality: 149969 bases at least 020 linest size: 150000; agarose-fp consers size: 150565; sum-of-contigs Quality coverage: 5.9 in Q20 bases; sum-of-contigs Quality coverage: 5.9 in Q20 bases; sum-of-contigs
                                                                                                          Center project Information
Center project name: L7490
Center clone name: 209_E_9
Center clone name: 309_E_9
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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9442 11373: contig of 1932 bp in length
11374 11473: gap of 100 bp
47058 47157: gap of 100 bp
47158 49227: contig of 2070 bp in length
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120721 150210: contig of 29490 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
1. 9341
/note="assembly_fragment
                                                         Web site: http://www-seq.wi.mit.edu
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/note="assembly_fragment"
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47158. 49227
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ALSYOLIS THORONOSOME 1 CLORE FP11-234D19, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Enkaryota, Metazoa: Chordata; Chamiata: Wertebruta: EsteleOstomi;
Mammalia: Estheria: Primates; Catarrhini: Hominidae; Homo.
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Cambridgeshire, CBL0 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hunquery sanger arouk Clone requests: clonerequest sanger acouk
on Jan 19, 2002 this sequence version replaced q::17154305.
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Best Local Similarity 106.0%; Fred. No. 3.5e-39;
Matches #7: Conservative 0; Mismatches 0: Indels 0;
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59343. .6500A
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120721, .150216
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Web site: http://www.sanger.ac.uk
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was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGPChr9
RP11-535M15 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VBCTOR: pBAce3.6
IMPORTANT: This sequence is not the entire insert of clone RR11-535M15 it may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-330M2 is at 140528 in this sequence. The true right end of clone RP11-330M2 is at 2000 in this
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                                                                                                                                                                                                                                                                                                                          Search completed: July 5, 2002, 06:24:06 Job time: 5959 sec
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ORIGIN
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1: /cyn2_6/pt.odata/2/ina/5A_COMH.seq:*

2: /cyn2_6/pt.odata/2/ina/5A_COMH.seq:*

4: /cyn2_6/pt.odata/2/ina/fa_COMH.seq:*

5: /cyn2_6/pt.odata/2/ina/fa_COMH.seq:*

6: /cyn2_6/pt.odata/2/ina/fa_COMH.seq:*

6: /cyn2_6/pt.odata/2/ina/pcTUS_COMH.seq:*
Spyriaht (c) 1994 - 2030 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                343533 seqs, 122814752 residues
                                                                                      nucleic search, using sw model
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Japop 56.9 , Gapext 60.0
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Maximum DB seq length: 2000060000
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Perfect score:
Sequence:
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67 23	20	4.7	80595	7	US-09-078-294-3	~`
7.4	4.9	4.6	1663	7	US-09-499-884-11	Sequence 11, Appl
57. 5	¥	4,5	1 48 1	a	US-08-454-557C 49	Sequence 49, Appl
47 5	X T	ري د.	1481	~	US-08-340-426p-49	÷
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September 1 April 1 September 2 April 1 Septem		Indets 0; Caps
	RESULT 1 19.68-776-088-21 1 Sequenc 21, Application %5/28776-88 1 Sequenc 21, Application %5/28776-88 1 Patent No. 572-873 1 Sequenc 21, Application %5/28776-88 1 Sequenc 21, Application %5/28776-88 1 Sequenc 21, Application %5/28776-87 1 Sequenc 21, Application %5/28776-87 1 Sequenc 21, Application %5/28718-88 1 Sequenc 31, Application %5/28718-88 1 Sequenc 31, Application %5/28718-88 1 Sequenc 31, Application %5/28-15 1 Sequence 31, Application %5/28-15 1 Sequenc	Section 73: 34: 1: count. From No. 2.70-20; [not of the country of
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5.7%; Score 61; DB 1; Length 1656;
100.0%; Pred. No. 1.7e-20;
Live 0; Mismatches 0; Indels
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US-08-465-981-2/C
Sequence 2, Application US/08465981
Fatent No. 5874415
GENERAL INFORMATION:
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                           FILLING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065001
TELECOMOUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALDBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,981
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
APPLICATION DATA: US/08/324,465
                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
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Best Local Similarity 100.0
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
Massachusetts
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US-08-324-465-2
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ZIP: 02110-2804
                      RY: U.S.A.
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                    COUNTRY:
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Patent No. 5565334
GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Kufe, Donald
TITLE OF INVENTION: GENE TRANSCRIPTION AND
TITLE OF INVENTION: IONIZING RADIATION:
TITLE OF INVENTION: AND COMPOSITIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09145A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%; Score 77; DB 5; L4 100.0%; Pred. No. 2.7e-28; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
REGISTRATION NUMBER: 37,345
REFERENCE/DOCKET NUMBER: B35792CIPPCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 214-939-4600
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 Dasse pairs
                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STRRET: 1201 Elm Street, Suite 4500
CITY: Dallas
                                                                                                                                                                                                               Lung Cancer Marker
22
                                                                                                                                               Sequence 21, Application PC/TUS9509145A GENERAL INFORMATION:
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PCT-US95-09145A-21
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                        837 CAGTGAGCCGAGATCAC 853
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Matches 77; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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COUNTRY: US
ZIP: 75270-2197
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                                                                                                           RESULT 2
PCT-US95-09145A-21
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                                                                                                                                                                                                                                                                                                                                                                                                Guery Match 5.7%; Score 61; DB 2; Length 1556;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 51: Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-1963-11915-2/C

Sequence 2. Application PC/TUS9311915

GENERAL INFORMATION:

APPLICANT: Kile, Donald

APPLICANT: Abe, Miyako

TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING

TITLE OF INVENTION: EXPRESSION IN PETITHELIAL CELLS

NUMBER OF SEQUENCES: 8
                                                                                           REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
RETERECORMUNICATION INPORMATION:
TELEPHONE: (617) 542-5070
TELEPK: 200154
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 562 or 552X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTAMRE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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FILING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/999,742
FILING DAIE: December 31, 1992
AFFORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fraser, Janis K. REGISTRATION NUMBER: 3.
                                                                                Fraser, Janis K.
                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
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                                                                                                                                                                                                                                                                                                                        OPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
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STREET: 220
"Y: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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802 ayaqqetqaqqeqqaqaatcqettqaaeerryyyaqqqaqttqeaqttqaqqeeqaqt 861
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                                                                                                                0; Caps
                                                                        Length 1656;
                                                                                                                :: Indels
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kufo, Donald
APPLICANT: Abo, Myako,
1111E OF INVENTION: GENE TRANSCRIFTION AND
1111E OF INVENTION: O'NIZING KAETALION: METHOLS
1111E OF INVENTION: AND COMPOSITIONS
NUMBER OF SEQUENCES:
CORRESSER: FISE & ROCHARGON
STREET: 225 Franklin Street
                                                                    Cuery Match
Best Local Similarity 100.0%; Prod. No. 1.7e+200
Matches 61; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER FEADABLE FORM:
MEDIUM TYPE: 3.5" DISKELLE, 1.44 MD
COMPUTER: 118P PS/Z Model 502 or 558X
OPERATING SYSTEM: MS-PWS (Version 5.1)
SOFWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324.465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08324469
Patent No. 5565334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALFORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
; TOPOLOGY: linear
PCI-US93-11915-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-324-465-5/c
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US-68-324-465-5
                                                                                                                                                                                                                            862 C 862
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802 ggaggctgaggcaggagaatcgcttgaacccgggaggcggaggttgcagtgagccgagat 861
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Sequence 7, Application US/09268992

Fatent No. 634251

GENERAL INFORMATION:

APPLICANT: Chen, H.

APPLICANT: Chen, H.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS

FILE REFERENCE: 7853-138

CURRENT APPLICATION NUMBER: US/09/268,992

CURRENT FILING DATE: 1999-03-16

EARLIER APPLICATION NUMBER: 60/106,056

EARLIER FILING DATE: 1998-10-22

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 61; Conservative 0; Mismatches 0; Indels
    EXPRESSION IN EPITHELIAL CELLS
                                                                                                           CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00530/065WO1
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFRENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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PCT-US93-11915-5
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APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.7%; Score 61; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.7e-20; Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00530/065002
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
FILLING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
FILLING DATE: December 31, 1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US93-11915-5/c; Sequence 5, Application PC/TUS9311915; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REPERENCE/DOCKET NUMBER: 0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                Sequence 5, Application US/08465981
Patent No. 5874415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
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    862 c 862
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Harity 100.0%; Pred. No. 1.5e-20;
Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Staels, Hart
APPLICANT: Croston, Gleun E.
APPLICANT: Miller, Stephen G.
IJILE OF INVENTION: MODULATORS OF OL GENE AND
IJILE OF INVENTION: SCREENING METHOUS FHERIFOR
COPRESPONDENCE: 48
COPRESPONDENCE ADDRESS:
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"MPUTER: IBM Compatible

CPERATING SYSTEM: IHM P.C. D'S 5.0

SOFTWARE: FASLENT OF WINGOWS VERSION 2.0

CURRENT APPLICATION DATA:

FILING DATE: MATCH 19, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219: 9:071-2000
OMFUTER PEAGABLE FORM:
OFFUT VOR: 3.5" DISKette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 219/U75
TELECOMMUNICATION INFORMATION:
                                                                                                           : LOCATION: all n positions
: OTHER INPORMATION: n-a, c, q, or t.
US-69-268-992 7
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October 40, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   > Sequence 4, Application US/U8618100B
: Patent No. 6968976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/510,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: April 5, 1995
APPLICATION UNBER: 08408-534
FILING LATE: MATCH 20, 1995
ATTORNEY/ASSNT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 2, 1995
JMBER: 08/418,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
SIREET: 63 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Briggs, Michael R. APPLICANT: Aiwerx, Johan APPLICANT: de Vos, Prot APPLICANT: Staels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32, 327
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TELEFAX: (213) 955-0440
FELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DAIA:
                                                                                           NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Rich:
REGISTPALION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: August
APPLICATION NUMBER:
                                                      ORMANISM: Home sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Los Angeles
                                                                                                                                                                                                      Opery Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFURMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
SEL 11. Nº 7
LEN 3TH: 724-4
                                                                                                                                                                                                                                                                                                                                                                                          Db 15952 t 15952
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                                TYPE: DANA
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No. 4.5e-17; Matches 54; Conservative 0; Mismatches 11.1e.s
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DESCRIPTION: Sequence between exent; and exent
Patent No. 6068936
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Best Local Similarity Police, Prol. No. 4.7
Matches 58; Conservative © Missaertes
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Patent No. 6262*33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(579)
OTHER INFORMATION: n - A.L.C or 3
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANI: Brady, Mutthew G
INFURMATION FOR SECTION : 4: SHOUTHWIN CHARACTERISTICS: LENGTH: 10.044 Association of MYPH. During of a strain STRANDHINESS: Single
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                                                     NAME/KEY: misc_feature
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US-09-242-948-1/6
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US-08-618-10UB-4
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LEN3TH: 179
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                                                                                5.0%; Score 54; DB 4; I
100.0%; Pred. No. 4.2e-17;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
....has 52; Conservative
                                                                          Ouery Match
Best Local Similarity 100.0
Matches 54; Conservative
        ; ORGANISM: Homo sapiens US-09-210-748A-3
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LOCATION: 858..863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: sig_peptide
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LOCATION: 880..891
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US-09-247-155-141
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US-08-973-544-1
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GENERAL INFORMATION:
APPLICANT: Hermeking, Helko
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
FILE REFERENCE: 1107.77810
CURRENT APPLICATION NUMBER: US/09/210,748A
CURRENT PILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/069,416
PRIOR PILICATION NUMBER: 1997-12-18
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
LENGTH: 7680
                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,948
FILING DATE: 25-Feb-1999
CLASSIFICATION: <Unknown>
                                                              (Outside USA)
INVENTION: Protein Targeting to Glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.0%; Score 54; DB 4; L
100.0%; Pred. No. 4.2e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ashbrook, Charles W
REFERENCE/DOCKET NUMBER: 5485-01-CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313 996-5215
TELEFAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,107
FILING DATE: 30-AUG-1996
                                                                                                                                         ADDRESSEE: Warner-Lambert Company
STREET: 201 Tabor Road
CITY: Morris Plains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: 4238..5176; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-242-948-3
Printen, John A
Saltiel, Alan R
Warner-Lambert Company,
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Patent No. 6335156
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LENGTH: 5789 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      ZIP: 07950
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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Best Local Similarity 100.0
Matches 54; Conservative
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US-09-210-748A-3/c
                                                                                TITLE OF
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6086 TCCCAGCTACTCGGGAGGCTGAGGCAGGAATCGCTTGAACCCGGGAGGCGGA 6033
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Bouguelert, Aymeric
APPLICANT: Bouguelert, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET: 021A
CURRENT APPLICATION NUMBER: 05/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,273
EARLIER FILING DATE: 1998-08-10
SARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 141
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 4.147

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 5.6999980925514

OTHER INFORMATION: seq LLIFFGKLLVVGG/VG
                                                                                                                                   Sequence 141, Application US/09247155A Patent No. 6312922
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Gaps
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Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0;
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NUMBER F SEQUENCES: 4

CHRESH-NIGHTE ADDRESS:
AGURESSEE: NIKALIN-, MURRAY & CRAM LIB-SPECE: NIKALIN-, MAKMELSIEIN, MURRAY & CAGASEE: NIKALIN-, MAKMELSIEIN, MURRAY & CAGASEE: NIKALIN-, NW. SUITC 400, G ST. LOBBY TIY: Washington

CONTINEY: LOS

COMPUTE: DG

COMPUTE: PRAMARE: PARK:
MENDIOM IVEE: Flopy disk
MENDIOM IVEE: Flopy disk
MENDIOM IVEE: Flopy disk
MENDIOM IVEE: RAP PC compatible
OFFERALING SYSTEM: PLOSS/MS-25'S
SOFFERALING SYSTEM: PLOSS/MS-25'S
SOFFERALING SYSTEM: B-DEC-1997
CLASSIFICATION NUMBER: BC-1997
FILLING DATE: 20-JUN-1995
PRICK APPLICATION DATA: PS-105511.6
PRICK APPLICATION DATA: PS-105511.6
FILLING DATE: 20-JUN-1995
FILLING DATE: 20-JUN-1995
PRICK APPLICATION DATA: PS-1000
FILLING DATE: AD-JUN-1995
APPLICATION NUMBER: EP-9510201.9
FILLING DATE: 20-JUN-1995
APPLICATION NUMBER: EP-9510201.9
FILLING DATE: 20-JUN-1995
APPLICATION NUMBER: EP-9510201.9
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APPLICATION NUMBER: EP-9510201.9
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801 gggaggctgaggcaggagaatcgcttgaacccgggaggcggaggttgcagtgagccgaga 860
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                                                                                                                                                                                                                861 teacaccactgeactecageet 882
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Best Local Similarity 100.
Matches 82; Conservative
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Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Sacres, M.B., Tan, P., Thierry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra,
Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                             N76766 494 bp mRNA linear EST 28-JAN-1997 yv45c05.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:245672 5' similar to contains Alu repetitive element;, mRNA
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1; CalTech Human BAC Library D" 121 c 131 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 845 Std Error: 0.00 Seq primer: reverse ET
                                                                                                                                                                                              808 tgaggcaggagaatcgcttgaacccgggaggcggaggttgcagtgagccgagatcacacc 867
                                                                                                                                                                                                                              108 TGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCACACC 167
                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:245672"
/clone_lib="Soares fetal liver spleen lNFLS" \
                                                                                                                Length 536;
                                                                                                                                                        Indels
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0
                                                                                                                    7.9%; Score 85; DB 12; 100.0%; Pred. No. 7.4e-32;
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                         868 actgcactccagcctgggcgacaag 892
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N76766.1 GI:1239344
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/ncte="Vector: pampl0; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of bNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PNN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMPl0 by the UGG-cloning method (Life Technologies). Average insert size is 600 powers.
                                                                                                                                         AA224995 423 bp mRNA linear EST 21-AUG-1997 nc34c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010024 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissaue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissaue Procurement: W. Mo.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 423;
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Pred. No. 8.2e-30;
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Insert Length: 600 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 353.
Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Pr2"
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/lab_host="DH10B"
47 TCACACCACTGCACTCCAGCCT 26
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100.0%;
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Figure 1: Folert Strausberg, Ph.D.
Figure 1: Folert Strausberg, Ph.D.
Figure 1: Folert Strausberg, Ph.D.
Figure 1: Folert Strausberg, M.D., Foltjob Ch.aqui, M.D.,
Figure 1: Foregreenti. W. Marston Linehan, M.D., Rodijob Ch.aqui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
chM. Library Preparation: David B. Krizman, Ph.D.
chM. Library Preparation: David B. Krizman, Ph.D.
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Mammalia: Butheria; Primates: Catarrhini: Hominidae; Homo.
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/db_xref="taxon.9606"
/clone="Ince:199134"
/clone_"Ince:199134"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="bl108 (phage resistant)"
/note="Organ: lymph; Vector: poTBT; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                       Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Hedde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J. E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: John Quackenbush
The Institute for Genomic Research
  National Institutes of Health, Mammalian Gene Collection (MGC)
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Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                       image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 446.
Location/Qualifiers
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100.0%; Pred. No. 8.9e-27;
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                 Unpublished (1999)
Other_ESTs: bblle04.yl
Contact: Robert Strausberg, Ph.D.
                                                                                       Email: cgapbs-r@mail.nih.gov
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Plate: 107
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contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Prayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 564 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 387.

Location/Qualifiers

Ir. 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AM30e09.S1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:953896 similar to contains Alu repetitive element; contains element FX MER29 repetitive element; mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="mAGE resequences, MAGE"
/note="Vector: pBluescriptsKm"
108 c 150 g 117 t 1 c
                                                                                                                                                                                                                                                                                                                         Query Match 7.0%; Score 75; DB 9; La
Best Local Similarity 100.0%; Pred. No. 8.7e-27;
Matches 75; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:953896"
Location/Qualifiers
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/db_xref="G|:18027812"
/translation="WAGGVOYGSWPHWWYGLETLPGLVKKSCYKTAKLLLVQRSPTFL
ATGSTFLEDHFSWEREGGGGGGWFWFHLPSSGTSQTLRGTQNLHSWGAQFTGGLLL.
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota, Metazoa; Chordata; Craniara; Vertebrata; Futeicostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2820)
Zhou.X.M., Zhang.P.P., Jiang.H.Q., Huanq.Y., Oln.W.X., Zhao,X.T.,
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Zhou,X.M., Zhang,P.P., Jiang,H.Q., Huang,Y., Qin,W.X., Zhao,X.1.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wan, D.F. and Gu.J.R. Novel human cDNA clones with function of inhibiting cancer cell \mbox{Novel}
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 David Krizman,"
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                                                                      Length 569;
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Local Similarity 100.0%; Pred. No. 6.5e-27;
Les 75; Conservative 0; Mismatches 0;
                                                                        Score 75; DB 9; L
Pred. No. 8.6e-27;
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library was constructed by
168 a 133 c 162 q 106 t.
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                                                                      7.0%; Score 75; DB
llarity 100.0%; Pred. No. 8.6
Conservative 0; Mismatches
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/db_xref="taxon:9606"
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1. .2820
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/organism="Neumo sapiens"
/db_xiet)*(axin_cycon"
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4170607.xl NCL_CGAP_0026 Home sapiens 5.NA clone IMAGETB01813 3
similar to contains Alu repetitive element contains element IJPS II
repetitive element 5. mRNA sequence.
BE051830 242 bp mPNA linear EST 99-JPN-2-09.
RCI-RCIO54-271199-314-gtl F15254 Homo supiens CDNA, mRNA sequence.
BE0561830
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Mammalla: Eutheria: Primates: Pataribin: Hominidae: Homo.
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Brazii
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Proc. Natl. Acad. Sci. U.S.A. 97 (7) -191-496 (2008)
200268
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100.0%; Pred. No. 3.26-26;
ative 0; Mismatches ::
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Email: asimpson@ludwig.crg.kr
                                                                                                                                BEOWIRYO,1 61:8406480
EST.
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
      scanning the human genome
Proc. Natl. Acad. Sci. U. S.
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AW072006.1 GI:6027004
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                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 44 Std Error: 0.00
Seq primer: -40ml3 #wd. Er from Amersham.
Location/Qualifiers
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Adams, M.D. and
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                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 358)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
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/clone_lib="NCI_CGAP_Ov26"
/sex="female"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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Best Local Similarity 100.
Matches 74; Conservative
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3688
Fax: (206) 616-3687
Email: jWallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 590 row: P column: 12
Seg primer: SP6
Class: BAC ends
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Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites" 3 others
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="plate=590 Col=12 Row=p"
/clone_lib="RPCI-11 Human Male BAC Library"
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Pred. No. 2.9e-26;
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                                                             Contact: Mahairas GG, Wallace JC,
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/organism="Homo sapiens"
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Location/Qualifiers
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Pun frajlodytes DNA, clane: PIB-148P2L.K, genomic survey servence. Alferto.
Alferto.
ANFERTO.
GNS, GNS Conserved.
close the transport by: Greg Cennon, Ph.D.
TAN Sequencing by: Washinaton University Second Sequencing Sector
TANA Sequencing by: Washinaton University Second Sequencing Sector
Those distribution: NCI-SAR Colone distribution information can be
read 'horough the L.M.A.S.E. Consort om/LLM. at:
****-bio.lnd.gov/bbrp/imaae/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                        T 37]; double-stranded cDNA was ligated to Fro RI adaptors (Pharmacia), digested with Not I and cioned into the Not I and Fro RI stres of the modified pP714 Tector. Library is normalized, and was constructed by Beatomasses and M.Patima Bonaido."
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Pan froqlodytes male lymphoblast DNA, clone_lib:PTH chimpanzee Male
BAC Library clone:PFH-148F21.R.
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Mammaisa, Entheria, Primates, Catarrhini, Hominidae, Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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/lab_host<"OH168"
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Totoki,Y., Wafacabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Mathodal Institutes of Health Marmathr and Soldering (MPP)
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Obfact Mator Stansberg, Ed.:
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/clone_lib="NIH_M51_2""
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Best Local Similarity (vol.0%) Pred. No. 2.70 (2)
Matches 74: Conservative 0; Mismatches (9)
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/db_xiet "taxon: "Fee"
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Consensus quality: 133398 bases at least Q30
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Estimated insert size: 136595; sum-of-contigs estimation
Guality coverage: 4.95 in Q20 bases; agarose-fp estimation
Quality coverage: 4.91 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* of the gaps between them are based on estimates that have
provided by the submittor as soon as it is available and

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 2163: contig of 2162 bp in length

* 2263: 5221: contig of 2961 bp in length

* 5224 5323: contig of 18976 bp in length

* 5324 5323: gap of unknown length

* 5324 5323: contig of 9876 bp in length
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130223: gap of unknown len
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Center: Joint Genome Institute
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source FEATURES

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 Score 4797;
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 61.2%;
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Best Local Similarity 99.6
Matches 7717; Conservative
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27254 ATGITCITCIGGITCCASCAFAWACACHSTWWAA HAAN WIGALGGAAAAAACACA 2733 27434 TAAACCAAGGCTTAAAGAATAGTAGATTGATTGATAAAAAASSS SSTAAASSAASGA 27455 27494 AGATGTTTTFCCCTCCTTTACTTTFCTANATAATTTTTALTTTGGATAAAFAAACSCTG 27553 27674 AGCAAGASGIAFOTIFFOTIACASTATITICAAASAASSAAFAAA TIGAGAAATIGIS 272 93 26894 GGCGATGACTGTCACATGTAGGGAGAGGGGGATRSACTGGGSTTGGTGGTGTAGGGGGGG 24453 27314 GCTAGICLCCCTTCCTCCACCAGCAACCTITSTIACTGALAATGAATTGAATTGACTATT 27373 27154 AGGCAGGAGAAAAGGCALTGAASATSSSSCASAAGSAAAGSAAAGCAATTT 2725-222] gaqtaqeeeruettqaqqqeeertaqeetaaanaatbqaaauuqqqqeeeretee 2283 2281 aggagagtcatctgcagygctacccaurachdagtaaytaaytaacaqaqtaaccaaau 246 234] aug-magagagamaayumattimaaqmattayammat-mayayimatgimaatin 2398 2399 alditeiteitaatteeageatameaeaemantimaaatuaameteatgeaagaaaaema 2458 2459 antaminiteretienteraneamentitumitaniamiaatumamitemiatt 2918 2579 tabaccaagnoottaaaadaatuaqaaatuaqtamattrabajaaqrifootaaquqaaqa 2038 2639 agailotititteeteetilaetiiletasaataa'iti'atiiluualaaalaaaeeete 2698 2699 atabatqaqaacccacucttcccaaqqccaaqcttttqttttuuquua.gatcctccqtc 2758 2101 tiganiginicacnantolgaailaladalunnyqqaniichicatolomanocanaca 216. 2819 agecaaqayutatettiteeetaeayetteteaagaaaaaaaanoeentaaattata 2838 2879 appellagasacaccyaqaqaychqachcccs/ullibiasacachcallagautifatar 2938 2939 atggaaggcaggaggaggactgagautuctztattattattatttattttattit 2998 2999 taaaaaaartqqat-raqrovvarit,tqaataraaaaafqaaaatuuqaaattfqcata 3057 3058 acageaet tyaacutet qaaaquueeeganueet uurugeet ii inquqeaeee 1117 3118 ettetanetagabategebaagattaannanaaaaaq <177 6 G 90 QQ 35 25 Š g 9 d 5 â . ? 9 5 90 Š CF ŏ 20 3 g Š 3 ŝ qq 3 QC. ô q ŝ Ē 3

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qq	29951	CAGCAGCACAGGGCTGGGGGGCTCCCGGAGCTGCGTGCCAGCCGGGGTTTCGGCCAGA 30	
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jan 15, 2002 this sequence version replaced gi:18152648.
  32530 GTTTGCTATTTAAAGTATCTCAAAACATATCCATAAGAATACATATGAATGGAACTAATT 32589
                                                                                                                                                                                                                                                                                                                                                                                             AL669821 144702 bp DNA linear HTG 31-JAN-HOMO sapiens chromosome 6 clone XXbac-116A1, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4 5
Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 144136 bases at least Q40
Consensus quality: 144299 bases at least Q30
Consensus quality: 144299 bases at least Q20
Insert size: 144402; sum-of-contigs
Insert size: 167909; 14.3% error; agarose-fp
Quality coverage: 10.72x in Q20 bases; sum-of-contigs Quality
coverage: 9.55x in Q20 bases; agarose-fp
                                                                                                                                                                   gtttgctatttaaagtatctcaaaacatatccataagaatacatatgaatggaactaatt
                                                                                     coccacatgtgaaccatatgtgtacatatgcccatatttaaaaatacaaattctgcacctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bPG116A1
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AUTHORS
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AL669821
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                  Submitted (17-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 25, 2002 this sequence version replaced gi:18250865.
                                    SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 136657; sum-of-contigs
Insert size: 115180; 6.1% error; agarose-fp
Quality coverage: 7.81x in Q20 bases; sum-of-contigs Quality
coverage: 9.23x in Q20 bases; agarose-fp
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                                                                                                  HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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7624 41360; contig of 33737 bp in length
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Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 134624 bases at least Q40
Consensus quality: 135417 bases at least Q20
Consensus quality: 135772 bases at least Q20
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                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
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41461. .47515
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                                                                                   AL669924.4 GI:18375903
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                                                                                                                                     Homo sapiens
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Direct
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AL669924/c
                                DEFINITION
                                                                                                                                   ORGANISM
                                                                                                                                                                                                   AUTHORS
TITLE
                                                                 ACCESSION
                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                     JOURNAL
                                                                                                  KEYWORDS
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                             47616. .52829.

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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                0; Mismatches
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accctagatytagactagcagtgctacaacctcaagtctcagaagtatgtcactagacc 	agccaaaaalagutgctatatcattaagagagtaaaaatgcaaaccacagaca 	ttattcacaataagcatalaaccacaqgggactoctatct 	aatcaataaqaaaagqcaaagatttaaacagqcactt 	aaatsaataaacatiigaaaagaiccicaaticactagtiatiagggaaaggtsa 	algagagocccacgeeecacgeertaa 	ačegaatyttqeaaqqatqegaaaaactqeattttdt 	aaatotgtacaaccaqqttggaaacqotgaqtaqaatgtactot 	Lgaalatoatatgatccagcaattctactcctagaaattlacccaacagaatgtgtaaa 	aatteatag 	aaaaavtqqaaactacccaaatgtccatcagcagagaatggcqataaacagtagcat 	acataaigaaatgittcgacagcaatgaaagiagctagct 	ttgaacctcacaaacatatactaaqtaaaattatcagacacaaaggtgtatatac 	ahitagatacatgtgaagtctgaaacaggcaaagctattctgttgttagaagtcaga 	agttantgeertgeegggaaacagaacteagagggettagtagetactggtaatgtt 	acticetgaactgcatgctagtgagcagctgttattitgtgcagtoctgtdt 	qqaqtLaaaaqttcccccaaaatcaqaaqtqtLcaqcaagtgqaaqcaaqtacctuct 	ggactiggggacttaggggatctcataartigicacaggracaagcaagccacc
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7.7 Db	dy 5b	Cy Db	5 6 E	75 199	C OY	ag ag	0.7 Opp	9.y Dp	0y 0b	0.7 Db	oy ob	े दे डे	5 3	AS QC	2 ag	중 원	, qn

2100 56076 TIGGCIGTCTCACACTCTGAATTATAAALPPPRAACTIG CTACACTTVAACCACACACA SECTA FILE HITTELLE HITTELLE HITTELLE HELLE ELLE ELLE HELLE HELLE HELLE HELLE HELLE HELLE FERRE SSR AGGCCAGGAGGAGGAGGATGTCAASCATTGGAATGGASCATTGGASCA | FETTILLE . 85. 55417 26.75 55536 AGAEGITITECCTECTITACTITECTACAGIAATITITATIITAGAIAAATAAACCETG 55477 204 2101 tiggetgteteaeraetetuaaftalaarjonmadaetientiafulmeraeeraeaea 216g 2281 aggagagteatetecagggetaceramantuagtaanteanteantaantaan 240 234] agn-cannanacannnatheannathumhmanuait-uannathumhmathteeanne 2398 2399 atgittettettqqtteeaqeataqeacacqutucaaatuaar...stealgeaaqaaaacaca 2458 2459 getaglictecetteetenaneageaanetifauttactaaluataa*haaatteaetatt 2518 2519 illititititititaactaauqetqaqataalu*rasarqserarqqqqaaqqaaqqaaqqcr 2978 2639 agaigtttttccctccttactttctacadaattffaltngalaaalaaacceta 2698 2699 ataaatqaacccacqettteecaaqqeeaquetsialillaatquatgeteeteegte 2758 2759 aucaqtiggaqtaafccaqautgatcccaqqqqarcaaqcaaqteqtqqa 2818 2819 aggraagaqqatettinedananetinidasagastinosienenataattqtq 2878 2879 additiguaaacaccaaaaaqdctganthenatulalaasoothattataa 293k 2939 atugaaqueaqqaaqqaaqetqaqaatqettattattattattatti 2498 1927 graaggeaggatteaggaalagetgagantttleesagtar aertggteerageteree 1981 teteceaettetaatgaangunagtanayetettagajaagagentgagteeta ggdgatgactgtcanat ctaqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq 2221 gagtagdddtgagarrentgagertgagatagaatagagaaneetennetenneten 1861 ticitgeontaagtageatriceeagagteaggateeaggaulguttuugageaugg 2579 taaaccaaqqccttaaaqaatqaJaaqaarfoattoaaassagcctootaaqqqaa 1921 56196 9. Pp 55 25 26 9.0 9.0 9.0 9.0 99 09 Db 6 G 90 οy g 5 G ô gg 0.y 0.y g Š q ó qq $\stackrel{\textstyle \sim}{\circ}$ a 8 q

	ata 3057 ATA 5511	aca 3117 ACA 55057	acag 3177 ACAG 54997	tgca 3237 TGCA 54937	ctag 3297 CTAG 54877	rcac 3357 cac 54817	ggac 3417 GGAC 54757	ggaa 3477 GGAA 54697	tggg 3537 IGGG 54637	cccg 3597 CCCG 54578	ggcg 3657 GGCG 54518	ccta 3717 CCTA 54458	ata 3777 ATA 54398	lacg 3837 ACG 54338	.gcg 3894 GCG 54278	caca 3954 CACA 54218	aaac 4014 AAAC 54158	gcac 4074
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25022	299	3058	3118	3178	3238	3298	3358 54816	3418	3478	3538	3598	3658	3718	3778	3838	3895	3955	4015
Ę	7 of a	Qy Db	Qy Dp	oy Op	Qy Dp	Qy	Qy Db	Qy Db	Qy	Qy Dp	Qy Dp	Qy Db	Qy Dp	QY Db	Qy Db	Qy Dp	Oy Dp	δy

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where uniterences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNDEP; Information the WORNDEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 http://www.sanger.ac.uk/rojects/chromosome at the http://www.sanger.ac.uk/rojects/c_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 http://www.sanger.ac.uk/rojects/chromosome and the http://www.sanger.ac.uk/rojects/chromosome and the http://www.sanger.ac.uk/rojects/c_elegans/wormpep This sequence
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Human DNA sequence from clone RPI1-149B7 on chromosome 13, complete
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Submitted (05-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBD10 15A, UK. Ermail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jan 8, 2001 this sequence version replaced gi:11863351.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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54157 GTGTGTGTTCCCAGAGCAGCTCCAGAGTGCGGCAGGGACGCTGGGGGGCGGCGGGGGGGCAC 54098
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                                                GI:12044488
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Wall, M.
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JOURNAL
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http://www.sanger.ac.uk/HGP/Chr13
spl1.14987 is from the library RECI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm

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Principal Control of 174537)

Since B. Linton. L. Nusheum, C., Lander, E., Abraham, E., Allen, N., Anderson, S., Baldwin, J., Barkerly, R., Beda, F., Bodus, S., Baldwin, J., Barkerly, R., Beda, F., Gastle, A., Gloepel, Y., Colancelo, M., Collins, S., Collymore, A., Cooke, P., Coderellano, K., Dewar, K., Domino, M., Dople, M., Fenestor, J., Ferrellano, K., Dewar, K., Pomino, M., Boyle, M., Fenestor, J., Ferrellano, K., Dewar, K., Domino, M., Boyle, M., Fenestor, J., Ferrellano, K., Stan, L., Karatas, A., Klein, J., Gordyna, S., Stan, D., Lovine, K., Man, L., Karatas, A., Klein, J., Landers, R., Leporkky, J., Lovine, R., Man, L., Karatas, A., Klein, J., Landers, R., Marpais, N., Merban, P., Medicia, J., Mornow, J., Naylor, C., Mornow, J., Naylor, C., Worman, J., H., Pelerson, K., Ferrelson, M., Medicia, J., Mornow, J., Naylor, C., Waymond, S., Riley, R., Friban, B., Ferrelson, M., Pelerson, C., Pelerre, N., Raymond, S., Riley, R., Friban, B., Ferrelson, M., Pisan, C., Doulara, V., Raymond, S., Riley, R., Friban, B., Ferrelson, R., Berrelson, 
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Bomo sapiens chromosome 11 clone RP11-805N8 map 11, WORKIN3 DRAFT
SEQUENCE, 13 unordered pieces.
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Sto.acovic.N., Subramanlan.A., Talamas.J., Tesfaye.S., Teodore.J.,
Tirreli.A., Vassillev,H., Viol.R., Vo.A., Wu.X., Wyman.L., Ye.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.864. 7.3790
/note-"Sequence from overlapping clone AL138380. Contains lobe single clone. Assembly confirmed by restriction diagrat. 7.8877
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Eukaryoka: Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheriu; Primates; Calarrhini; Hominidae; Home.
1. (bassa: 1 to 174537)
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VECTOR: pHALOS, the entire insert of clone RP11-149E7 The truelieft end of clone RP11-1.0KB is at 155804 in this sequence. The true tilth end of clone RP11-463MM is at 117835 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4375 athordaethaetegydaguetgaggeagaaaaaaategettaaaceegggagggaggjis 4434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinote "Single clone region. Assembly confirmed ty restriction dignst data." 49216 a 34741 c 33637 q 50236 t
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Local Similarity 100.08; Pred. No. 1.5e-4
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/db_xret "taxon.9606"
/chromosome."13"
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Smit, A.F.A. & Green, P. (1993) 1935
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Contact: sequence_sulaiss: as tenam swinmit.edu
Project intonadion
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 189492)

2. Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

2. (bases 1 to 189492)

3. Lattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

3. Pattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

3. Direct Submission

3. Submitted (13-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

3. Totokii. Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@qsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

3. Nove 22, 2000 this sequence version replaced gi:8119019.
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19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
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                                                Assembly program: Phrap; version 0.990329
Consensus quality: 184605 bases at least Q40
Consensus quality: 186235 bases at least Q30
Consensus quality: 187002 bases at least Q20
Insert size: 187692; sum-of-contigs
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Best Local Similarity 100.08; Pred, No. 1.56-42;
Marches 98; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                    27 187914; config of 100 bp.
15 188914; config of 1788 bp in length
15 188914; aap of 100 bp.
15 18945; config of 1478 bp in length.
1, 189447
             190 bp
3540 bp in length
                                                                                              100 bp
2619 bp in Pengit
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188615. .189492
/note="assembly_fragment"
a 3789c c 38104 g 57868 t
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10016="assembly_fragment"

136855. | 145978

70016="assembly_fragment"

146079. | 152076
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/organism."Homo sapieus"
/db.xrel "taxon:9606"
/chromosome "11"
/map."Hil24"
/clone."RFH:755,5,7"
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55510. .77235
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165799. .771331
/note="assembly_tragment"
171432. .175338
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179768. 184307
/note="assembly_fragment"
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110185. .118234
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152177. .159408
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/note*"assembly_fragment"
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186127, .187914
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118335. .127661
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174568 179757; qap ot 19
79768 184707; contiq of 35
184708 184407; qap of 10
18408 186026; contiq of 26
185027 186126; qap ot 10
185127 187944; contiq of 14
1878015 188914; dap of 10
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runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                   Center project name: H NH055F01

Sequencing vector: M13; 81%
Sequencing vector: plasmid; 19%
Chemistry: Dye-primer ET; 81% of reads
Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 171727 bases at least 0.0
Consensus quality: 17727 bases at least 0.0
Consensus quality: 177384 bases at least 0.0
Insert size: 192000; agarose-fp
Insert size: 179141; sum-of-contigs
Quality coverage: 3.63 in 0.20 bases; sum-of-contigs
Center: Washington University Genome Sequencing Center
Center code: WUGSC
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137365: gap of unknown length
181047: contig of 43682 bp in length.
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g of 7526 bp in length
f unknown length
g of 8041 bp in length
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10037: contig of 19225 bp in length
10137: gap of unknown length
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contig of 8772 bp in length
gap of unknown length
contig of 8149 bp in length
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of 6670 bp in length
                             Web site:http://genome.wustl.edu/gsc/index.shtml
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unknown of 6480 h
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of 4500 b
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of 6165 h
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of 4031
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of 2980
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of 5825
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of 4717
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1933: gap of unknown
3870: contig of 1937
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contig of 3066
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/db_xref="taxon:9606"
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137366
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/chromosome="11" /clone="RP11-555F1" 1. .1833

misc_feature

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Homo sapiens chromosome 2 clone RP11-134G21, WORKING DRAFT SEQUENCE, 3 unordered pieces.
AC092602 AC060810
AC092602.1 GI:14916107
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 154633 TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGC 154574
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Pred. No. 7e-41;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1912 others
                                                                                                                                                                                                 14284. 17263

/ note="assembly_name:Contigl8"

17364. 23188

/note="assembly_name:Contigl9"

23289. 28005

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32706. 38209

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38310. 44789

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44890. 55559

/note="assembly_name:Contig23"

/note="assembly_name:Contig23"

/note="assembly_name:Contig23"

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59286 .67326
/note="assembly_name:Contig26"
67427 .73591
/note="assembly_name:Contig27"
73692 .82463
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82564. .90712
/note="assembly_name:Contig29"
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137366. 181047
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/note="assembly_name:Contig30"
110138. 137265
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1934. .3870
               1934. .3870
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10153. .14183
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Submitted (19.30).2001) Jenome Sequencing Penter, Washinst as
University School of Medicine, 4444 Forest Park Farkway. St. 52318,
Mo 6.81@8, USA
                                                                                                                                                                                    on Jul 19, 2001 this sequence version replaced dislud9855.
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96634: cont.a of 142133 bp in length.
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elone_end:SP6
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A. Control of A. Olille 42462
HTG.
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Mammalia: Butheria: Primares; Jajarrinn: Buninidae; Homo.
] (bases: to 17449)
Sulston.J.E. and Materst L.S
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University, 4444 Firest Fack Ashara, St. Lids, Missoull (1)-6,
en Jan v. 2002 (Gis Serpaton Section 1), and the 144708 (
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Waterston, F.H.
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The RECEIL homen BAP library was made 19 m the blood of one male donor, as described by oscorpawa,K., Weed LY., Zhao,B., Frenger,E

SOURCE INFORMATION:

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4449 cacaccactgcactccaqcctqqqqqquna 4477

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AW264166 (NID:96640982) xq84g02.x1"
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6695. .6986
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7938. .8310
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0; Mismatches 0; Indels 0;
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8649. .8692
/rpt_family="MIR"
8852. .8872
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5024. 5134
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9226_.9308
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/rpt_family="MIR"
8322. .8648
/rpt_family="Alu"
8439. .8471
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9923. 9969
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10185. 10223
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Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics. Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
WECTOR: PAMCe3.G
WEIGHBORING SEQUENCE INFORMATION:
                                                                                                                              The clone sequenced to the left is RP11-717A5, the clone sequenced to the right is RP11-439L14. Actual start of this clone is at base position 1 of RP11-513019; actual end is at base position 904 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002. 2082

//note="similar to Sus scrofa EST BI339210 (NID:g15032493)"

2214. 2455

//note="similar to Sus scrofa EST BI343196 (NID:g15036485)"

2372. 2455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2625, 2783
//note="similar to Sus scrofa EST BI343196 (NID:g15036485)"
2625, 2783
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1466. .1576
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/note="similar to Sus scrofa EST BI339210 (NID:g15032493)"
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8796. 3987
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                                                                                                                                                                                                             Data from AC096715 was used to finish this clone, AC016753.
Location/Qualifiers
1. 175694
/organism="Homo sapiens"
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/chromosome="2"
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/note="match to EST AW374393 (NID:g6879047)"
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Anote="match to EST AW293024 (NID:g6699660)"
3796, 3888
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/note="match to EST AL040160 (NID:95409125)"
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(NUD:914293096)"
1298. 3599
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3946. .3989
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/noce=sinilar to Homo sapiens EST BG312620
(NID:g14293096)"
2611. .2783
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/rpt_family="(CACCC)n"
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992. .1088
                                                                                                                                                                                                                                                                                                                                /clone="RP11-513019"
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529. .590
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/rpt_family="HY1"
1754. 2087
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4746. .5130
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1925 bp in length
78 kp
1948 bp in length
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contin of 14477 kp in length
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129282 149602: contid of 20421 bp in length
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2860 2959; dap of leg bp 2860 2959; dap of 1229 hp in legath 2255 5354; contiq of 2295 hp in legath 5255 5354 app of 130 hp 5355 8788 888; contiq of 3444 hp in length 88789 8888; dap of 160 hp 11519; contiq of 2479 hp in length 11520 11519; dap of 126 hp in length 11520 11519; dap of 3479 hp in length
                                                                                                                                                                                                                        20079; qap ol 15° bp
23673; contig of 4594 kp in length
23773; qap of 17° bp
22287; contig of 45/4 bp in length
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24: contiq of 5116 bp in lenuth
gap of lum bp
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/clone_lib="RPC1-11 Himman Male BAC"
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/note="assembly_tragment"
33549. .39008
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2960. 5054
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.27787. .77287
.7note="assembly_tradcent"
.27388. .4448
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/note="assembly_tragment"
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Znote-"assembiy_fragment"
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81128 91377: contig of
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1. .178508
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117038 117137; qap of
117138 129181; conti
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149703 178508: conti
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/map="2"
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27388 - 33448: conf
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                                                                ACH23440 178508 bp DNA linear HTG 03-MAX-2009
HGMC sapiens chromosome 2 clone RPII 748NI3 map 2, WORKING DRAFI
SEQUENCE, 23 unordered pieces.
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                                                                                                                                                                                                                                                 Evkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaia; Pitcheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 17808)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13: M7815; 100% of reads
Sequencing vector: M13: M7815; 100% of reads
Assembly program: Phrap: version 0.960731
Consensus quality: 164472 bases at least 040
Consensus quality: 171343 bases at least 040
Consensus quality: 171343 bases at least 020
Insert size: 171000; agarose-fp
Insert size: 171000; spin-of-contigs
Ouality coverage: 4.5 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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1449 2859: contig of 1411 bp in length
                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, R. Homo sapiens chromosome 2, clone RPI1-748N13
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Certer clone name: 748_N_13
                                                                                                                                                                                 HIG; HTGS_PHASE1; HTGS_DRAFI.
                                                                                                                                                        AC023040.3 GI:7684460
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                                                                                                                                      AC023040
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                                          AC023040/c
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Center code: WUGSC
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                                                         Waterston, R.
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Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
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HOMO sapiens BAC clone RPl1-510C1 from 2, complete sequence.
AC010984
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Du,F., Maupin,R. and Hawkins,M.
The sequence of Homo sapiens BAC clone RP11-510C1
Unpublished (2001)
3 (bases 1 to 191540)
Waterston,R.H.
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/note-massembly_fragment"
149703. 178508
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Waterston, R.H.
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Matches 89; Conservative
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscepawa K., Woon, P.Y., Zhao, B., Frengen, E., Tateno.M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com) vbcTOR: pBACC3.6 NEIGHBORING SEQUENCE INFORMATION:
Submitted (19-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 191540)
                                                                                                                                                                                                               Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 19, 2001 this sequence version replaced gi:14349340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The clone sequenced to the left is RPI1-397H17, 2000 bp overlap: the clone sequenced to the right is AC023040. Actual start of this clone is at base position 29090 of RPI1-109E12. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST BE350015 (NID:99261868) ht07h01.x1"
1028. .1385
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                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
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/note="match to EST AL043002 (NID:95422428)"
1034. .1504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
-------- Summary Statistics
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/db_xref="taxon:9606"
/chromosome="2"
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55. .455
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/moie="maich to EST AI424427 (NID:94270358) teSSII1.x 13691891 /rp!=family:"AT_rich"	1925. Zubs. 70010-78milar to Sus scrota ESI BI185548 (Nibisi4659957)" 1408. 1769.	/#670i.ml // Molte "similar to Homo sapiens EST A1826796 (NEL 95447467) WK56d04_x1"	14261763 /note-"similar to Homo sapiens EST AI805283 (NID:45391849) re3-408 vi	1426. 1763 /note-"similar to Homo sapiens ESI BF027338 (NID:q10735050)"	19481763 Widther="similar to Homo Sapiens ESI A1762531 (NIL:45178198) Widthoft x1"	1557. 1903 /note-"similar to Bos taurus ESI BF035486 (NID:31:e75	2101 1128 Zhote-"CpG_island (%GC-65.6, o/e 0.70, #CpGs 95)" 2101.	21822545 27812642 "match to EST AL040143 (NID:q5409108)" 25112642	/rpt_tamily."Alu" 26512961	/rpt_tamily="Alu" 29362962	7.pv.dmlij (FAA)n 3298 - 1516 /hotes"match to ESI BE14403、(NIL::q8606757)"	3559. 4286 760te "march to ESI BF680099 (NID:q11953994)" 860t	/rpt_family "L1" 4754 AB20	#724:#022 //octe=match to ESI BF948699 (NID:q12355974)" 4777 5075	/note="similar to Homo sapiens EST BF750345 (NIU:q12077021)"	49405074 // // // // // // // // // // // // //	(NED:49810/3/)" 4943 . (507) Anote-"motich to FST BEGROUSS /NED:010377532/"	4950. 5074 //note="match to EST BF948699 (NID:q12365974)"	4991. 5105 /note-"match to EST AW206302 (NID:q6505794)"	5284. 5583 5284. similar to Homo sapiens EST AA654287 (NID:425 6783-68.	5442. 5438 7402. 5438 7/00.02 Similar to Homo sapiens EST AI798417 (NIS:q5353889)	54.5497 500 5897 700.e-"match to EST BF948699 (NID:q12365974)"	58305897 Zoote="Similar to Homo sapiens EST AI798417 (NII:453 Lr54a04.x1"	5830. 5897 Znote "navrh to: EST BP966155 (NII/.q12377534)" 5847. 5892	to ESI AA640869 (Ning2566119) m24an	/note-Tmatch to EST AA987270 (NIN:g3172634) os[ib 2. 2866. 1897 /note-Tmatch to EST BE67703; ANTH-G119500263"	.6428 "match to EST	64826570 /rpt_lamily-"MERL_type" 7024862
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Ento 151865 151#45 bp 1.NA linear HTG 20-SEP-2700 chromosome H clone RP13-204E9 map H, WORKING DRAFT unordered pieces. Metazóa, Chordata: Zramiata: Vortebrata: Enteleostori: Etheria: Primates: Zatarthin.: Brinidae: Homo. Eo 181865. Inton.: Nusbaum.C. and Lander.F. 0.ce-"similar to Home sapitors ESI AV7x21s5 IDig1E843740)" Pictabliz Pt_tabliz Pt_18540 "Alu" 09s_28640 austri to ESI AA704640 (NIP:q2713958) ausili0.10" F__tan_1; "..." 59. _r44P pr__tan_1; "(1)..." 26. _873 pr__tam_1; "Alu" 19. _863 19. _e63 36. _to64 igagaat egelit qaaeee bagagagagagaaa tattacaatgaageegaagat 4448 sing to status 1.18. Schröder 18 de 1. marsh 191540: celoko Erra, No. M. Cerri, parens volor de Mismatches e Hoders e CCASCCTGGSTCTACA 415 3 readerigadenase 4477 GI:101985+0 BASEL: HIGS_DRAFI. pt_tamily="L1" 799, .918* pt_tamily "M:R" 813. .7899 rpt_family-"..." 898. .7994 rpt_family "..." 656. .8439 3. .7572 t_tamiiy "Li" 3 (0) (1) 7447 ative

COMMENT

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Center: Wellcome Trust Sanger Institute
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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AUTHORS
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Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Tadiamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Trawars,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (07-WAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 20, 2000 this sequence version replaced gi:7188875.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 151000; agarose-fp
Insert size: 150565; sum-of-contigs
Quality coverage: 5.9 in 020 bases; sum-of-contigs
Quality coverage: 5.9 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center close name: 209_E_9

Center close name: 209_E_9

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 146689 bases at least Q40

Consensus quality: 149124 bases at least Q20

Consensus quality: 149969 bases at least Q20
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87420 87519: gap of 100 bp
87520 97716: contig of 10197 bp in length
87520 97716: contig of 10197 bp in length
97717 120620: contig of 22804 bp in length
120621 120720: gap of 100 bp
120721 150210: contig of 29490 bp in length
150721 150310: gap of 100 bp
150311 151865: contig of 1555 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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9442 11373: contig of 1932 bp in length
11344 11473: gap of 100 bp
11474 1473: gap of 3584 bp in length
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/db_xref="taxon:9606"
/chromosome="8"
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JOURNAL
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FEATURES

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DNA linear HTG 30-JAN-2002 RP11-234D19, *** SEQUENCING IN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (24-3NN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 19, 2002 this sequence version replaced gi:17154305.
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/clone="RP11-209E9"
/clone_lib="RPCI-11 Human Male BAC'
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100.0%; Pred. No. 2.1e-36;
Live 0; Mismatches 0;
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45019 a 30571 c 30486 g 44487 t
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                                                                                                                                                                                                                                                            120721. 150210
/note="assembly_fragment"
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/note="assembly_fragment
                                                                                  1. .9341
/note="assembly_fragment
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Homo sapiens chromosome 1 clone
PROGRESS ***, in ordered pieces.
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vector_side:left"
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AL590113.7 GI:18250776
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Best Local Similarity 100.
Matches 87; Conservative
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Hall,R.
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us-09-761-466-4.rge

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Unier communication (16-JAN-2002) Wellcome Irust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
CA
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Human DNA sequence from clone RPI1-535M15 on chromosome 9, complete
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Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142527)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insert size: 165292; sum-of-contigs
Insert size: 165022; 3.1% error; agarose-fp
Quality coverage: 6.57x in Q20 bases; sum-of-contigs Quality
coverage: 6.98x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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100.0%; Fred. No. 2e-36;
Live 0; Mismatches 0; Indels 0.
                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 66% of reads
Chemistry: Dye-terminator Big Dye; 38% of reads
Chemistry: Dye-terminator Big Dye; 38% of reads
Consensus quality: 165175 bases at least 040
Consensus quality: 165265 bases at least 040
Consensus quality: 165284 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:00114"
49350 a 33980 c 33334 g 48628 t
Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Home sapiens"
/db_xref="taxon:9606"
/chromosome="]"
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/clone_lib="RPCI-11.1"
1. .165292
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                                                                                                                                   Center project name: bA234D19
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AL589843.9 GI:18250502
H1G.
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Best Local Similarity
Matches 87; Conserva
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only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by hids quality data (i.e., placed quality 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least, one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction diest, The following abbreviations are used to associate primary accession numbers size in the feature table with their source latibases: En:, EMBL: Sw., SWISREPTI ITT: TERMIN. MP.: WYAMPEP: Information on the WORMPEPE
                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/~elequis/wormpep This sequence
was generated from part of barderial clune configs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP11-535M15 It may be shorter because we sequence overlapping sections only once, except for a short everlap. The true left end of clone FP11-350M2 is at 146528 in this sequence. The true right end of clone FP11-350M2 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group. Further information can be found at http://www.sander.ac.uk/BG/Y/in. Repl.555MB is from the library RPCJ-11.2 constructed by the aroup of Pieter de Jong. For further details see
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les 85; Conservative 0; Mismatches 5;
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Run on:

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July 6, 2002, 05:15:15 : Search time 249.41 Seconds (without aliquments) 8041.750 Million ceil updates/sec

US-09-761-466-4 7838 1 ctmgaqmmcaqqaqttmaq Title: Perfect score:

....daataaaaeqqntqaaann 7848 Gapop 50.0 , Gapext, 60.0 ·LIGO_NUC Scoring table: Sequence:

383533 seqs, 122816752 residues Searched:

Word size :

767066 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 9 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

/cgnz_6/ptiodata/2/ina/5A_n.MH.seq:*
/cgnz_6/ptiodata/2/ina/5B_0MH.seq:*
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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Restit. No.	Score	Viery Match	Viery Match Lenath DB	DB	1D	Description
,	77	1.0	1363	-	US-98-776-088-21	Sequence 21, Appl
.7	77	1.0	1463	u^	PCT-US95-09145A-21	-
~	6, 1	3 3	1656	-	US-08-324-465-2	
7	19	90.0	1656	7	US-38-465-981-2	Sequence 2, April
ري ن	6.1	8.0	16.56,	u-	PriT-1894-11915-2	i
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Ţ	6.3	0.8	72604	4	US-09-268-992-7	r
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23	54	C.7	7680	4	US-09-210-748A-3	~
	2.5	0.7	8-51	4	US-09-247-155-141	7
<u></u>	25	0.7	5581	4	US-58-973-544-1	
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r	L'	7	246240	.74	US-58-724-394A-ZU	
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77	4.4	0.6	3664	4	US-09-499-884-11	_
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Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 61; Conservative 0; Mismatches 0; Indels
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APPLICANT: Rufe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00530/065001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                        SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,465
                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
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225 Franklin Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08465981; Patent No. 5874415; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-324-465-2/C

Sequence 2, Application US/08324465

Patent No. 556534

GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Kufe, Donald
TITLE OF INVENTION:
TITLE OF INVENTION: IONIZING RADIATION:
TITLE OF INVENTION: AND COMPOSITIONS
TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09145A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: John A. Harre
REGISTRATION NUMBER: 37,345
REERERENCE/DOCKET NUMBER: B35792CIPPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 base pairs
                                                                                                                                                                                                                    TITLE OF INVENTION: Lung Cancer Marker NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSE: RICHARDS, MEDLOCK & ANDREWS STREET: 1201 Elm Street, Suite 4500 CITY: Dallas
                                                                                                                                                      Sequence 21, Application PC/TUS9509145A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               STATE:
COUNTY:
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
4435 cagtgagccgagatcac 4451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4435 cagtgagccgagatcac 4451
||||||||||||||||||
                                  837 CAGTGAGCCGAGATCAC 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   837 CAGTGAGCCGAGATCAC 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                              RESULT 2
PCT-US95-09145A-21
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                                                                                                                                                                                                                                                                                                                                                          STATE: TX
COUNTRY: U
                                                                                                                                                                                                      APPLICANT:
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RESULT

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double

linear

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4389 ggagget gaggeaggagategettgaaceegggaggeggaggttgeagtgageegagat 4448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9311915
GENERAL INFORMATION:
APPLICANT: ALG, DOBALD
APPLICANT: ALG, MYDAG
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATI
TITLE OF INVENTION: ENHESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb CUMPUTER: 1BM PS/Z Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPertect (Version 5.1) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K.
REGISTATION NUMBER: 34,819
REPERRYEATOCKET NUMBER: 00530/065W01
TELECOMMUNICATION INFORMATION:
                                                                                                                   00530/065002
          FILING DATE: December 31, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                         HEGISTRATION NUMBER: 34.819
REFERENCZ/DCCKET NUMBER: 00530
FELECOMBINICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
TELERX: 200154
INFORMATION FOR SEQ ID NO: 2:
SRQUENCE CHARACTERISTICS:
LENGTH: 1656
  vetober 17, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-5070 (617) 542-8905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IELEX: 200154
INF-PHATITIN FOR SEQ ID NO: 2
SEGUENCE CHARACTERISTICS:
LENGTH: 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DIS
                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: double
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FILING DATE: Octobe APPLICATION NUMBER:
                                                                                                                                                                                                                                                                             TYPE: nucleic aci
STRANDEDNESS: dou
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
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PCT-US93-11915-2/c
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                                                                                                   Jesuth 1656;
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100.0%: Pred. No. ( .ee-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kuie, Conald
APPLICANT: Abe, Miyaka
APPLICANT: Abe, Miyaka
TITLE GF INVENTION: TONIZING RADIATION: METHOLS
TITLE GF INVENTION: TONIZING RADIATION: METHOLS
TITLE GF INVENTION: AND SOMFOSTITIONS
TITLE GF INVENTION: AND SOMFOSTITIONS
OFFICE OF SECURIORS: 8
CORRESPONDENCE ADDRESS:
                                                                                                 0.8%; Score 61; DB 5; ; dilarity 100.0%; Pred. No. 6.3e-15; Conservative 0; Mismatches .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MADION TYPE: 75° Diskette, 1.44 ME
COMPUTER: THE PS/2 Model 502 or 55x
OPERATING SYSTEM: MS-L/OS (Version 5.1)

COHENNI APPLICATION DAIA:

APPLICATION NUMBER: US/08/324.4F
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Best Local Similarity 100.0%; Pred. No. 6.4
Matches 61: Conservative 9: Mismutches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
                                                                                                                                                                                                                                                                                                                                                                                    US-08-324-465-5/c
; Sequence 5, Application US/08324465
; Patent No. 5565334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/JOCKET WINDSEL: 6653
TELEGORMUNICATION INPORANTION:
TELEFAX: (617) 542-5970
TELEFAX: (617) 542-6970
TELEFX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CIRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14,835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Jamis
REGISTRATION NUMBER:
                                                                                                                     Best Local Similarity
Matches 61: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
STRANDEDNESS:
; TOMMLOGY: line
PCI-US93-11915-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY:
US-08-324-465-5
                                                                                                                                                                                                                                                                 4449 C 4449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                         309 C 309
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APPLICANT: Chen, H.
APPLICANT: Chen, H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/0106,056
EARLIER FILING DATE: 1998-10-28
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.8%; Score 61; DB 5; Length 1725; Best Local Similarity 100.0%; Pred. No. 6.3e-15; Matches 61; Conservative 0; Mismatches 0; Indels
    EXPRESSION IN EPITHELIAL CELLS
                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00530/065WO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/999,742
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: December 31, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09268992
Patent No. 6342351
                                                                 E: Fish & Richardson 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/FOCKET NUMBER: 001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                  STATE: Massachusetts
  TITLE OF INVENTION: EX NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                 ADDRESSEE:
STREET: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
PCT-US93-11915-5
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Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 61; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
                                                                                                                                             Sequence 5, Application US/08465981
Patent No. 5874415
GENERAL INFORMATION:
APPLICANT: Kute, Donald
APPLICANT: ADE, Miyako
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00530/065002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
FILING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8

FORTUGE 1915-5/c
Sequence 5, Application PC/TUS9311915
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 005
TELECOMMUNICATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        X: U.S.A. 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                Boston
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                                                                                                                         US-08-465-981-5/c
4449 c 4449
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                                          309 C 309
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                                                                                                                                                                                                                                     Length 72604;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Briggs, Michael R.
APPLICANT: Auwerx, Johan
APPLICANT: Auwerx, Johan
APPLICANT: Staels, Bart
APPLICANT: Staels, Bart
APPLICANT: Troston, Gleen E.
APPLICANT: Troston, Gleen E.
APPLICANT: Miller, Stephen G.
TITLE OF INVENTION: SCREENING METHODS THEREFOR NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  Query Match 0.8%; Score 61; DB 4; Lk Best Local Similarity 100.0%; Pred. No. 4.7e-15; Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERALING SYSTEM: IBM P.C. D.S 5.0
SOFTWARE: FactSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: March 19, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071-2066
COMPUTER READABLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: October 30, 1995
APPLICATION NUMBER: 08/510,584
FILING DATE: August 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: April 5, 1995
APPLICATION NUMBER: 08/408,534
APPLICATION NUMBER: 08/408,534
FILING DATE: March 20, 1995
AITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 219/075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEXX: 67-3510
                                                                                                        NAME/KEY: modified_base
LOCATION: all n positions
. OTHER INFORMATION: n=a, c, g, or t
US-09-268-992-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08618100B
Patent No. 5058975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/558,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Flith Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEIOR APPLICATION DATA: APPLICATION NUMBER:
                                         TYPE: DNA
OPGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RY: U.S.A.
90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: Ma
J ID NO 7
LENGTH: 72604
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 15952 t 15952
                                                                                                                                                                                                                                                                                                                                                                                                         Oy 4448 t 4448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-618-100B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oy - 4389 gqaaqortgaqqcaqqaqaatcqcttqaaccymqqaqqqaqttaqqqqqqqqqqqqqq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4382 etaetegggaugetgaducaudagaateurtidaannongdaageduageduage 4435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signi: :
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0.7%; Score 54; DR 4; Length 579;

Best Local Similarity 100.0%; Pred. No. 3.8e-1.;

Matches 54; Conservative 0; Mismatches 11, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VIVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: OF 1977 (2018) OURRENT APPLICATION NUMBER: US/09/725.111 CURRENT APPLICATION NUMBER: US/09/725.111 EARLIER APPLICATION NUMBER: US 60/088.R31 EARLIER APPLICATION NUMBER: US 60/088.R31 EARLIER FILING DATE: 19/98-06-16 NUMBER OF SEQ ID NOS: 850 SUFINARE: FRALES FOR TOWN OF 18 SOFTWARE: 1845.B50 SUFINARE: 1845.B50 TOWN OF 18 STATES FOR TOW
                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Sequence between exon 1 and exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score (8) DP 3; Lt
Pred. No. 8.26-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%: Pred. No. 6.2
60: Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT Endeqe, Wilson //
APPLICANT Steinmann, Rathleer E.
APPLICANT Asile, Jon H.
APPLICANT Hurdess, Christopher C.
APPLICANT Hurdess, Christopher C.
APPLICANT Carroll III. Eddic
APPLICANT Carroll III. Eddic
APPLICANT Carroll III. Eddic
APPLICANT Leris, Manan
APPLICANT Lewis, Marcia E.
APPLICANT Lewis, Marcia E.
APPLICANT Schiegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 741, Application US/1932811:
Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01HER INFORMATION: n = A.T.C or G
US-09-328-111-741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09242948
; Patent No. 6252057
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANI: Brady, Matthew J
                                                                                  LENGIH: 10684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_teature
                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                         6068976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-328-111-741/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULI 12
US-09-242-948-3/c
                                                                                                                                                                                                                                        FoPoloGY:
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-618-100B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 579
                                                                                                                                                                                                                                                                                                                                                                                   Pateut No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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4376 teceagetactegggaggetgaggeaggagaategettgaaeeegggaggegga 4429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4375 atcccagctactcggggaggctgaggcaggagaatcgcttgaacccggggaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08973544
Patent No. 6338950
GENERAL INFORMATION
EAPPLICANT: WEISS, Elisabeth
TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
                                                                                           0.7%; Score 54; DB 4; Le
100.0%; Pred. No. 3.1e-12;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Le
2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
TITLE OF INVENTION: Complementary DNAS
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER PLILNG DATE: 1998-02-09
EARLIER PLILNG DATE: 1998-04-13
EARLIER PLILNG DATE: 1998-04-13
EARLIER PLILNG DATE: 1998-04-13
EARLIER PLILNG DATE: 1998-09-10
EARLIER PLILNG DATE: 1998-09-10
EARLIER PLILNG DATE: 1998-09-10
EARLIER PLILNG DATE: 1998-09-10
EARLIER PLILNG DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 52; DB 100.0%; Pred. No. 2.2
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 4.117
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 5.6999980925514
OTHER INFORMATION: SEQ LLLFFGKLLVVGG/VG
                                                                                                                                                                                                                                                                                                                                              Sequence 141, Application US/09247155A Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                 Best Local Similarity 100.0
Matches 54; Conservative
  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: polyA_signal
LOCATION: 858..863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 4..447
FEATURE:
                                                                                                                                                                                                                                                                                                                           US-09-247-155-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 880
US-09-247-155-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
       ; US-09-210-748A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 891
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US-08-973-544-1
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                  qq
                                                                                                                                                                                         δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 GGAGGCTGAGGCAGGAGAATCGCTTGAACCCCGGGAGGCGGAGGTTGCAGTGAGC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
APPLICANT: Hermeking, Heiko
APPLICANT: Wogelstein, Bert
APPLICANT: Wogelstein, Bert
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107.77810
CURRENT APPLICATION NUMBER: US/09/210,748A
CURRENT FILING DATE: 1998-12-15
PRIOR PILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: DNA
                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,948
FILING DATE: 25-Feb-1999
CLASSIFICATION: <UNKNOWN>
                                                                   (Outside USA)
TITLE OF INVENTION: Protein Targeting to Glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 54; DB 4; Ler
100.0%; Pred. No. 3.2e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: AShDrock, Charles WEFERENCE/DOCKET NUMBER: 5485-01-CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313 996-5215
TELEPA: 313 996-1553
INFORMATION FOR SEC 1D NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,107
FILING DATE: 30-AUG-1996
                                                                                                                                                              ADDRESSEE: Warner-Lambert Company
STREET: 201 Tabor Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 4238.,5176
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                             Warner-Lambert Company,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09210748A Patent No. 6335156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5789 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
Printen, John A
Saltiel, Alan R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                              CITY: Morris Plains
                                                                                                                 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           ZIP: 07950
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.7%
Best Local Similarity 100.0
Matches 54; Conservative
                                                                                                                                                                                                                                                            ns
                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-210-748A-3/C
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Best Local Similarity 100.0%; Fred. No. 2e-11;
Matches 52; Conservative 0; Mismatches 0; Indels
NUMBER OF SECUENCES: 4
CORRESPONDENCE ALGRESS:
AUDRESSEE: NIKALDO, MARMELSTEIN, MURKAY & GRAM ILP
STREET: 655 Filteenth St., NW. Suite 300, G St. Lobby
CITY: Washington
                                                                                                                                                     TIP: 20(05-5-10)

"MPUTER FREZEBILE FORM:

"COMPUTER FREZEBILE FORM:

"COMPUTER: 15M FC COMPATIBLE

"OPERATING SYSTEM: PC COMPATIBLE

"OPERATING SYSTEM: PC COMPATIBLE

"SUFTWARE: PATENTING LATA:

"APPLICATION DATA:

"ELING LATE: 18-DEC-19-7

"CLASSIFICATION: 445

PHOR APPLICATION DATA:

"PUT CLASSIFICATION DATA:

"PUT CLASSIFICATION DATA:

"PUT CLASSIFICATION NUMBER: PC 95109511.6

PHOR APPLICATION NUMBER: EP 95109511.6

PHOR PROFILE 20-10N-1995

PHOR PROFILE 20-10N-1995

PHOR PROFILE 20-10N-1995

PHOR PROFILE 30-30N-1995

PROFILE COMMUNICATION NUMBER: P8 441-7073

PELEPHONE: (202) 638-4810

INFERMATION PASSIFILES: LENGTH: 5581 base pairs

LEMSTH: 5581 base pairs

TOPPE: OPERATION PASSIFICE:

LENGTH: 5581 base pairs

TOPPE: OPERATION PASSIFICE:

"TOPOLOGY" linear
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MOLECULE TYPE: DNA (genomic)
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US-08-973-544-1
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Search completed: July 6, 2002, 20:18:21 Job time: 54186 sec

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    2002, 12:44:21; Search time 16495 Seconds
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10279.718 Million cell updates/sec

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Post processing: Listing first 45 summaries

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| cun2_6/ptodata/2/pna/US06_COMB.seq;*
| cun2_6/ptodata/2/pna/US08_COMB.seq;*
| cun2_6/ptodata/2/pna/US09_COMB.seq;*
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28	82	0.1	X,X	L ∵	US-4014 750-10045-2000	Sequence 2008, Ap.
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CURRENT APPLICATION NUMBER: PCT/USO1/01511
CURRENT APPLICATION NUMBER: US 60/176,419
PRIOR RILING DATE: 2000-01-16
PRIOR RILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FRASEQ for Windows Version 4.0
SOFTWARE: PRASEQ for Windows OF SEQ ID NOS: 20
US-60-212-350-4
US-60-213-348-12
US-60-229-514-27
US-60-229-514-29
US-60-12-664-69
US-60-212-664-69
US-60-212-664-1193
US-09-760-443-2106
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// OTHER INFORMATION: n =

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                                          TYPE: DNA
ORGANISM: Homo sapiens
PRIOR APPLICATION NUMBER
PRIOR FILING DATE: 2000
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APPLICANT: Lee, IRe W.
TITLE OF INVENTION: Cardiac-Cell Specific Enformation of the Month of the Mo
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; Sequence 3, Application US/09761466
; GEREAL INFORMATION:
APPLICANT: Lee, IKe W.
TITLE OF INVENTION: Cardiac-Cell Specific Series of INVENTION: and Uses Thereof;
TITLE OF INVENTION: and Uses Thereof;
CURRENT APPLICATION NUMBER: US/09/761;
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,4
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FASEEQ for Windows Version
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: DOLYMOLPHISMS in the Human Genome FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/05/534,3068
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tive 0; Mismatches 3;
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PRIOF FILING LATE: 2000-07-12
PRIOR PRIOR LOADS: 0000-07-12
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SCFIWARE: FastSEC for Windows Version 4.0
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CUBRENT FILLINT DATE: 2000/02/10
NUMBER OF SEQ ID NOS: 14.640
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GENERAL INFGRATION:
APPLICANT: Outlis, And to
APPLICANT: Lotace, Folory E.
APPLICANT: Klingler, Tod M.
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GENERAL INFORMATION:
APPLICANT: Beth Israel Deaconess Medical Center
TITLE OF INVENTION: Cardiac-Cell Specific Enhancer Elements
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 01948/069W02
CURRENT APPLICATION NUMBER: PCT/US01/01511
CURRENT FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 375
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Matches 375; Conservative
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CORGANISM: Mus musculus
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PCT-US01-01511-1
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APPLICANT: Lee, Ike W.
TITLE OF INVENTION: Cardiac-Cell Specific Enhancer Elements
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 101948/069002
CURRENT APPLICATION NUMBER: US/09/761,466
PRIOR APPLICATION NUMBER: US 60/176,419
PRIOR APPLICATION NUMBER: US 60/176,419
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASTERQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Falb, Dean R.
APPLICANT: HOLtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1175-001
CURRENT APPLICATION NUMBER: US/09/652,915
CURRENT APPLICATION NUMBER: 60/152,110
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-652-915-2592
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TYPE: DNA
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                                                                                                       Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : OTHER INFORMATION: Incyte ID No: CpG_991027_B15_masked_fa.Contid29958
0S-50-782-315-1254
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      Length 410;
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                                           Indels
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  Score 370; DB 25; I.
Pred. No. 1.2e-102;
                                               0;
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Best Local Similarity 100.0%; Pred. No. 4.1e-90;
Matches 329; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Klingler, Tod M.
APPLICANT: Stuve, Laura L.
TITLE OF INVENTION: CpG Island Polynucleotides
FILE REFERENCE: PX-0003 P
  Guery Match 4.7%; Score 370; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 370; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/50/182,316
CURRENT FILING DATE: 2000-02-10
NUMBER OF SED ID NOS: 14,630
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1254, Application US/60182316
GENERAL INFORMATION:
APPLICANT: Curtis, Anne L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Curtis, Anne L. APPLICANT: Lagace, Robert E.
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Query Match
Best Local Similarity
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LENGTH: 338
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APPLICANT: Pham, Miso The;
TILLE OF INVENTION: BUBAN CARDIAN CELL-MERIVE, POLYNOTENTINES
TILLE OF INVENTION: AND POLYPEPTIDES
NUMBER OF REQUESES: 46-90
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lénath 182;
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Fred, No. 4.16 4';
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100,08; Bred N., ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITM TYPE: Floppy Disk
COMPUTER: IBM PC COMPALID.e
COMPUTER: IBM PC COMPALID.e
SUFTWARE: Word PRITECT 6.0/5.1/MS-1948
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1374, Application US/UNA69881
GENERAL INFORMATION:
APPLICANT: Ublequench Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/U8/34.9.88
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NAME: Barbara J. Luther
REGISTRATION NUMBER: 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-855-0555
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Best Local Similarity 100.0
'-- 182; Conservative
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CLASSIFICATION: 536
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LENGTH: 182 base pairs
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STRANDEDNESS: single
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IMMENIATE SOURCE:
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SEQ ID NO 41534
LENGTH: 8965
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LENGTH: 457
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GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Bilegeane, Angelo M.
APPLICANT: Bils, Pamela K.
APPLICANT: Pham, Mino T.
APPLICANT: Pham, Mino T.
APPLICANT: Alilman, Jennifer L.
TITLE OF INVENTION: CARDIAC CELL-DERIVED POLYNUCLEOTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 1954
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 182;
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APPLICATION NUMBER: US/08/408,872
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Similarity 100.0%; Pred. No. 3.1e-45;
32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           E: INCYTE PHARMACEUTICALS, INC. 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: LUTHER, BARRARA J
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD-0032 US
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 855-0555
TELEFAX: (415) 855-0195
INFORMATION FOR SED ID NO: 494:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Word Perfect 6.1 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       STREET: 3330 HILLV CITY: PALO ALTO STATE: CALIFORNIA
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Best Local S
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APPLICANT: Mang, Tongtong
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Robert
APPLICANT: Klee, Jennifer
TITLE OF INVENTION: LUNG TUMOR-ASSOCIATED SEQUENCES AND METHODS OF USE
FILE REPERENCE: 210.121.580
CURRENT APPLICATION NUMBER: US/09/866,555
CURRENT APPLICATION NUMBER: US/09/866,555
NUMBER OF SEQ ID NOS: 20487
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 CCAAGIGICAAGACTCATCGAACIGIACACTITIGIICTAGGIACATIAGACCTCAAIAA 292
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC004PCT
CURRENT APPLICATION NUMBER: PCT/US01/01354
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 4206
SOFTWARE: Patentin Ver. 2.0
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US-09-866-555-406/c
; Sequence 406, Application US/09866555
; GENERAL INFORMATION:
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) LOCATION: (1)...(457)

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US-09-866-555-406
                                                                    APPLICANT: Harlocker, Susan L. APPLICANT: Wang, Tongtong
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PCT-US01-01354-41534
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Matches 98; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/764,905
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PRITE APPLICATION NUMBER: 60/175,265
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PRITE APPLICATION NUMBER: 60/174,365
PRITE PRIME APPLICATION NUMBER: 60/214,365
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GENERAL INFORMATION:
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PCI-CS: 1-01354-41534
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us-09-761-466-4.rnpm

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PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/235,214
PRIOR FILING DATE: 2000-09-16
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PRIOR FILING DATE: 2000-09-16
PRIOR PELICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/249,218
PRIOR PELICATION NUMBER: 60/249,218
PRIOR PELING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 60/249,218
PRIOR PELING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
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PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14
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PRIOR APPLICATION NUMBER: 60/232,398

Gaps ·. Length 8965; 0; Indels Query Match 1.3%; Score 98; DB 30; Best Local Similarity 100.0%; Pred. No. 1e-19; Matches 98; Conservative 0; Mismatches 0

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Search completed: July 7, 2002, 01:14:25 Job time: 45064 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result.	Score	Cupity Materi	owery March Denath DB	<u>:1</u>	<u>.</u>	Description
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normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library." 210~\rm c 204~\rm g 113~\rm t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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A1393753
A1393753.1 G1:4223300
EST.
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/lab_host="DH10B"
                                                                                                                                                          Pred. No. 3.8e-109;
                                                                                                                                        DB 10;
                                                                                                                                    5.3%; Score 415; DB 100.0%; Pred. No. 3.8 Live 0; Mismatches
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/db_xref="taxon:9606"
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libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DAA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAS from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clonelDs: Soares NBAF pool 1: 309384-310919, 323208-325895 Soares NBAFP pool 1: 145032-14735, 147720-148103, 148872-149255, 15002-150407, 151176-152327 Soares NBAFP pool 1: 758280-766583, 772104-774407 Soares NBHPA pool 1: 78820-766583, 772104-774407 Soares NBHPA pool 1: 783720-726407, 739080-740999 Subtraction by Bento Soares and M. Fetima Bonaldo."
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Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi

Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 308)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Dupblished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
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0; Mismatches 1;
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IMAGE:1625417 3', mRNA sequence.
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National Cancer Instituto, Cancer Genome Anatomy Project (GGAP),
This come is available royalty-tree through LLNL; contact the Indicating that the Charles and the Charles intornation. Insert Length: 1554 std Prior; 0.00 seq primer: -40ml3 twd. Ef from Amersham High quality sequence stop: 281. Livid quality sequence stop: 281.
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                                                                 Contact: Robert Strausberg, Ph.D.
Email: cqapbs-remail.ndh.gov
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,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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Seg primer: M13 Reverse
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Schoollenberg, K., Scales, M. B., Tan, F., Thierry-Med.J., Trecaskis, E., Underwood, K., Wohldman, P., Katerston, R., Wilson, R. and Marra, M. Schoofarton and and yield 2 be, and human expressed sequency thats Organize Pess. 6 (19), 807-828 (1994)
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chaaqui, M.D.,
Michael Emmert-Buck, M.D., Ph.D.
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This clone is available royalty-tree through LLNL; contact the
TMANE Consortium (intofimace.llnl.gov) for turcher informatism.
Insert Length: 845 Std Error: 0.00
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/clone_lib "Soares fetal liver spleen INFLS"
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                                                                                                                                                                                                                                                                Contact: Wilson KK
Washinston University School of Mydicine
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/sex "Male"
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/db_xret "taxomret" "
/elone "iMAGE:161 541"
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/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
94 c 108 g 68 t
                 /cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
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Local Similarity 100.0%; Pred. No. 3.2
Best Local Similarity 0. Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:2959134"
/clone_lib="NIH_MGC_8"
    /clone_lib="DCA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 376)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,

Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,

Cheng,Z., and Han,Z.

Homo sapiens cDNA DCA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV712092 AV712092 BCA Homo sapiens cDNA clone DCAAEG11 5', mRNA sequence.
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100.0%; Pred. No. 1.7e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 others
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-5080192.5
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 600 Std Error: 0.00
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constructed by David Krizman."
111 c 119 g 125 t
                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1010024"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                                                                                                                                                                           /dev_stage="45 years old"
/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCAAEG11"
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L Unpublished (1999)
Other Ests: bble64.yl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/hunl/iresources.shtml
Seq primar: -40Up from Gibco
High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                            bbliedw.xl NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2959134 3'
similar to contains Alu repetitive element;, mRNA sequence.
BE300645.1 GI:9184469
EST.
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/lab_host="H10B (phage-resistant,"
/lab_host="H10B (phage-resistant,"
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oliqo-dT priming. Directionally
cloned into ECORIXXhoI sites using the following 5'
adaptor: GGCAGGGG(). size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) 109 g 119 t [Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Length 376;
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Score 77; DB 9; L
Pred. No. 3.2e-12;
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Best Local Similarity 100.
Matches 75; Conservative
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Tumor Gene Index
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Hedde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, T.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackcrbush, J. or Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
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Similar to contains Alu repetitive element;contains element MER29
MER29 repetitive element ., mRNA sequence.
AA527961.1 GI:2270030
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            4375 atoccagotacteggaaggetgaaggeaggaategettgaaceegggaaggeggaggttd 4434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: John Duackenbush
The Institute for Genomic Research
Tel: 301 838 3528
Fax: 301 838 0208
Fax: 301 838 0208
Flat: johnq*tiqr.org
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Lissue Procurement: W. Marsten Interact, M.L., Rodrigo Chuaqui, M.D.,
Michael Emmert-Buck, M.D., PELIN,
CINA Library Arrayed by Ferome Systems Int., Grea Lennon, Ph.P.,
CINA Library Arrayed by Ferome Systems Int., Grea Lennon, Ph.P.,
DNA Sequencing by: Washinsten University Seasme Sequencing Center
Clone distribution: National Statishing of Int., Great Lennon, Ph.P.,
DNA Sequencing by: Washinsten University Seasme Sequencing Center
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the resulting FCR present showing in pAMPHO by the
UDS-choring method (Lite Techna Postes). Average insert
size is 600 bp. Noth: Not directionally choses. This
library was constructed by Lacid Krizman."
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Wan,D.F. and Gu.J.K.
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Mammalia: Butheria; Primates; Zararchin;: Hominidae; Homo.
NCI-CGAP http://www.ncbi.com.nih.acv/ac.cag.
National Cancer institute, Cancer Second Anatomy Frojert (CSAP).
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Zhou,X.M., Zhana,E.P., Jiann.B.,, Huant.Y., cla.W.X., Zhao,X...
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             Direct Submission
Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai
                                                                                                                                                                                                                                                                                                                                                              /translation="MYAGVGVGSWPHWWVGLETLPGLVRKSCYKTAKLLLVQRSPTFL
ATGSIFLEDHFSMEREGGAGFGMEVFHLPSSGISQTLLRSTQNLHSWCAQFTGGLLLL
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1 (bases 1 to 242)

2 (barcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Sodman, G.H., Carrealho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R., Reis, L.F., de Souza, S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCl-BT0254-271
199-014-glhkfa=1999-11-27&t4=1)
Seg primer: puc 18 forware
High quality sequence stop: 70.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/716 - Ludwig Institute for Cancer Research) profiles
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SUMMARIES

	Description		Genomic DNA #2 end	Human Nkx∠.5/Csx n	Heart muscle cell	Human Nkx2.5/Csx C	DNA encoding hCsx/	Human MINT 23 DNA C	DNA encoding novel	DNA encoding novel	Human neuroblastom
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                       The sequence represents the genomic sequence #2 of human Csx/Nkx2.5. The nucleic acid is useful for specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac cell-specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac specific enhancer elements may be used for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides cells originating in the human bone marrow or umbilical blood cells which are capable of differentiating into cardiomycoytes. These cells are useful in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction, and the study of cardiomycoyte differentiation. The present sequence is an oligonucleotide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cells capable of differentiating into cardiomyocytes and originating bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease
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                                                                                                                                                    Heart muscle cell; human; cell differentiation; heart disease;
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                                                                                                                         Heart muscle cell differentiation related DNA SEQ ID NO: 10.
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100.0%; Pred. No. 2.1e-181;
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                                                                                                                                                                                                                                                                                                                                                                                        Ogawa S,
                                                                                                                                                                                                                                                                                                                                                                                         Umezawa A, Hata J, Fukuda K,
                                                                                                                                                                                                                                                                                                28-DEC-1999; 99JP-0372826.
28-FEB-2000; 2000WO-JP01148.
02-NOV-2000; 2000WO-JP07741.
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P-PSDB; AAG64848.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adult bone marrow-originated cells capable of differentiating into heart muscle cells, applicable as remedies for various heart diseases particularly with damaged heart muscle accompanying degeneration
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Best Local Similarity 100.0%; Pred. No. 2.1e-181;
Matches 640; Conservative 0; Mismatches 0; Indels
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                            5228 egectarcegectateegggttanggeggegeggeetgeageetggetaeagrtgeae 5287
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                                                                                                                                                                                                                                                                                                                                                                    752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hCsx/Nkx2.5; cardiac enhancer; cardiac cell; cardiomyocyte induction; therapeutic; heart tissue; gene therapy; human; ds.
                      1868 grygnonryggnoycaacggaaggaaqcaqceqryntyctcttctcqcagangcaqqtcta
                                                                    agocacetigotgaaartoargocagocagutaaaalotggttocagaaorggocta
                                                                                                                                                                                           513 gaggagoutgetgaaacteacgteeangeaggteaagatetggtteeagaaeeggnorta
                                                                                                                                                                                                                                                   633 geogeogeotgeocgeaggategeggtyceagtgetgetgetgetgatggeaageoatgeet
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                                                                                                                                                                                                                                                                                                                                                    753 egectarecegectatecegggttacgggegegeggeetgeagectggetacagetgeac
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3288 tyccyctlaccccyccygectlccccaycycayccyycractyccyccyccaacaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4808 adaqetutgegedetucagaaqqeggtqqaqetgdaqaqaqqaqqaggeggacaaegedua
                                                                                                            1928 tgaggtggagggggggttgaaggaggaggggtactateggeoeggaaggegaenaget
                                                                                                                                                                                                                                                                                 qeogeconcidecoqeaqqaleqeqqiqeeaqtgeigqiqeqqqqaqqaaqeeatqeet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.
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The sequence represents the coding sequence of consider enhancer. ACSX/NK22.5 boundoyy domain B. The concern and a superful for sequences in a cardian cert. as an earlier marker of cardiomyceyte induction, e.g. for attimistic cert. as an earlier marker of cardiomyceyte induction. e.g. for attimistic cert. as an earlier induction. Genes expressed in the cardiac cert. Secondaries are useful for the translated expression of conservations. Cardiac Secondaries for the treatment of demanded heart tissue, cardiac specific enhancer elements may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methylated Cp3 island Amplification, MCA, CG1, 193 site; DNA methylation, restriction endomotolese; Small, isoscibinamen, Nmall mendiated entomotolese and advances and attached discorder; demontals attached sites astrocy, one diabetes mellitus; cell prollificative disorder; cancer; kidney; object breast; uterns; prostate; lund; leukarmia; quirblastoma; modulating agent; screen; hypermethy, atton; banan; methylated IN lumons; MINI; chromosome 5934-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 caaataggggagatttttttttttcttrccttttgtararm garcmacagoactgarag 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                 New cardiac specific cell enhancer elements, useful for specifically expressing qene in cardiac cell, as earlier marker of cardiomyceyte induction, e.g. for optimizing cardiomyceyte induction -
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                                                                                                                                                                                                                                                                                                                                                       Sequence 478 BP: 138 A: 129 G: 89 B: 122 I: - + the::
                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%; Score 47%; DB 22°;
100.0%; Pred, No. 3.5e-133;
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                                                                                                        Claim 21: Fig 50; 65pp; English
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                                                                                                                                                                                                                                                                                                            be used for gene therapy.
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The patent discloses a method known as Methylated CpG island (CGI)

Amplification (MCA) to identify methylated CpG sites (cytosine residues 5 of neighbouring guanine). The method uses a methylation-sensitive crestriction endonuclease Smal, that cleaves unmethylated CpG sites and cfs. it involves amplification of closely spaced methylated Smal sites. CGIs. It involves amplification of closely spaced methylated Smal sites. This method is used to determine the DNA methylation status of CpG sites in a given locus, in normal and neoplastic cells. It can be used for clasposis of age-related disorders, associated with methylation of CGIs, cell agostis of age-related disorders, associated with methylation of CGIs, cell agoster, e.g. cancer of the kidney, colon, breast, uterus, proslate and lisorders, astrocytoma and neuroblastoma. It is also used to evaluate the cell response to a methylation modulating agent. It can also be used to screen samples for the presence of hypermethylation colon cancer cell line, cacolon (Methylated IN Tumours) clone derived from colon cancer cell line, cacolon corresponds to the 3' noncoding region of the human homeobox gene, CSX.
                                                                                                                                                                                                                                                                                                                                                                  Methylated CpG island amplification (MCA) used to determine DNA methylation status of CpG sites in a given locus, useful for diagnosis of age-related disorders e.g. colon cancer and dementia -
                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 47; Fig 6F; 100pp; English.
                                                                                                                                               99WO-US25251.
                                                                                                                                                                                     98US-0106925.
                                                                                                                                                                                                                                                                                                                            WPI; 2000-365641/31.
                                                                                                                                                                                                                                                                                        Issa J, Baylin S,
                                                               WO200026401-A1
                         Homo sapiens.
                                                                                                                                           02-NOV-1999;
                                                                                                                                                                                                          10-MAY-1999;
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Toyota M;

5510 5511 tggggagaagggctcccaacatgaccctgagtcccctggattttgcattcactcctgcg 5570 295 235 0; Gaps 5391 cccgggattccgcagagcaactcgggagtgtccacgctgcatggtatccgagcctggtag 5451 ggaagggacccgcgtggcgcgcctgaccgatcccacctcaacagctccctgactctcg 4.6%; Score 312; DB 21; Lehgth 414; 99.5%; Pred. No. 7.8e-84; 2; Indels 0; Mismatches Matches 412; Conservative Local Similarity Query Match 5571 ò qq ò g δ g ò

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Sequence 414 BP; 80 A; 133 C; 133 G; 68 T; 0 other;

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Gaps

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Length 1335; Indels

2.9%; Score 194; DB 23; 100.0%; Pred. No. 6.8e-49; ive 0; Mismatches 0;

Best Local Similarity 100. Matches 194; Conservative

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Query Match

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as footoners involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Assetlay-Assaysset novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed security in the printed and product of intectly from MIPO
                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
5751 cgcagggcctgagatctggccgccattccgcgagccagggccgggcccggg 5804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in
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                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #14060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 14060; 103pp; English.
                                                                                                                                        BP.
                                                                                                                                      AAS78256 standard; cDNA; 1335
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABG14069
                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biodiversity
                                                                                                                                                                                                                13-FEB-2002
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polynucleotiles are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11), (11) is useful for generaling antibodies against it, detecting or quantitating a polyneptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in modical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The polypeptide and polynucleotide sequences have applications in diadnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention relates to isolated polynucleotide (I) and projection of the control of (II). The
                                                                                                                                         inading of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological artivity.
and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
                                                                       2877, amagggaaggtgamaggmodtggomaymamogetttettgemeeeacetggegel atd
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distinction, forensies, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; torensic; tood supplement; medical imaging; diagnostic; genetic disorder; s
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #3310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 1: SEW ID No 4310; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                          AAS67506 standard; cDNA; 729
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200008-0549167.
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24 AUS-2000;
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The invention relates to cover decres (AA) 1927 AA1974 () expressed in human reproblastoms. The nurtief acids are applicable as a probe of primer in diagnostim the premosts of tunes neared-strong, malignancy and susceptibility indicators or tunger markers to an it concer agents. The agent information for diagnostial products is a faired to factors similar to that for Newye and LEAA nears.
                                                                                                                                                                                                                                                                                                                                                                                                      Human; neuroblastoma: mallamancy: rancer; temour marker; Nemyc; TrkA; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids originating in gene expressed in human nearblastoma, useful as probe of primer in diagnostra products of human nearblastoma, malianancy and stsceptibility indicator or tumour market
Note: The sequence data for this pater, did not appear in the printed specification, but was obtained in electronic formul directly from Will at ftp.wipo.inf/pub/published_pot_sequences.
                                                                                                                                         Gars
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                                                                                                                                                                      1129 amatmaqqmcaatgettdumttmamttgmqmqmqmqm177
                                                                                                         Lenath 729:
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                                                           Sequence 729 BP; 168 A; 144 C; 195 3; 172 i.
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                                                                                                                                         Mismarches
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                                                                                                            lov. ok. Pre
                                                                                                                                                                                                                                                                               AA196691 standard; cDNA; 686 BF
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                                                                                                                        Loca, Similario
es 49; Conservativo
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hes 44: Conservative
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                                                                                                                                                                                                                                                                                                              AAI96691;
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RESULI 10 AAXOU679/c

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                                                                                                                                                                                                                                                                                                                                            This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAX00611-X00724; amino acid sequences AAX00611-X00724; amino acid sequences AAX00611-X00724; amino acid sequences and protein or gene therapy. Also, pathological
                                                                                                                                                                            immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; infilammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; disestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                            Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encode
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Ni J, Olsen HS;
                                                                                            Human secreted protein gene 69 clone HLDBQ19.
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Hu JS, Lafleur DW, Moore PA,
Ruben SM, Shi Y, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 229; 385pp; English.
AAX00679 standard; DNA; 1525 BP
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970S-0048095
970S-00480995
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970S-0041277.
970S-0041281.
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970S-0048069.
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                                                              (first entry)
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                                              25-MAR-1999
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30-MAY-1997;
30-MAY-1997;
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30-MAY-1997;
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30-MAY-1997
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ALD STANKE STANK

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conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia; therapy; ds.
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ess GA, Carter KC, Mucenski M,
Y, Moore PA, Komatsoulis G;
                                                                                                                                                                                                                                               Score 43; DB 20; Length 1525; Pred. No. 0.00049;
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                                                                                                                                                                   Sequence 1525 BP; 284 A; 502 C; 458 G; 276 T; 5 other;
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100.0%; Pro
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98US-0089508.
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                                                                                                                                                                                                                                                                                                             Conservative
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Olsen HS,
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Best Local Similarity
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16-JUN-1998;
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                                                                                                                                                                                                                                                                                                             43;
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Soppet DR,
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or by determining the presence of motations in the new genes, specific uses are described to each of the 94 genes, based on which itsenes they are most highly expressed in, and include developing products to the disposals or tredument of cancer, fumours, developmental absorbas that overal deficiencies, blood disorders, discusses of the immine system, autoimmune diseases, inflammation, altheries, Althelmer's action of sorders are disorders, arbitrates, as this ophreia, arthuits, as thus, pseriasis, sepsis, skir, disorders, atheroselerisis, disorders, intertions and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAV8614 to AAV86585 represent tragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tortal deficiency, blood disorder; immune system disorder; inflammation; outoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
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Endress GA, Carter KC, Mucenski M,
Shily, Moore PA, Komatsoulis G;
                                                                                                                                                                                                                                                                              Score 43; DB 21; Length 1525;
Pred. No. 0.00049;
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                                                                                                                                                                                                                                                                              e.68;
160,08;
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980S-0089508.
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980S-0089510.
980S-0090112.
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                                                                                                                                                                                                                                                                                                                 43; Conservative
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76 JUN-1998;
16-JUN-1998;
16-JUN-1998;
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22-JUN-1998,
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Best Local S
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AA297019 to AA297137 represent 94 isolated numbs sepreted protein areas. AAY86215 to AAX8633 are the secreted proteins dereaded by the 94 missingeness. This sequence represents a framework of the Luman secreted proteins. The deres and their corresponding secreted pelypedicies of seculi for preventing, from the 27 minutes of 12 medical could thus contested by determining the about AAY 12 medical could thus or by determining the about AAY 12 medical could thus or by determining the presence of a medical could be as a period of a many second by determining the presence of a medical could be a missing to the about AAY 12 medical could be a second after most highly expressed in and her open developmental abnormally residuations is a diagnostic or treatment of current temporals are represented.
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es 41: Conservative
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Best Logal S
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AAF16372;
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                          AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                              Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene expression product cDNA sequence SEQ ID NO:1933.
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 138 BP; 74 A; 25 C; 21 G; 13 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 42; DB 21;
100.0%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
Claim 1; Page 1346; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ14464 standard; cDNA; 208 BP.
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98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                                                                                                         42; Conservative
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7. Garcia PD, Ke
                                                                                                                                                                                                                                                                                                 the present invention.
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                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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AA214464/C
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comprising the sequences given in AA212532 to AA21779. Also described is method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell cancerous state of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA21232 to AA217779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct therapeutic purposes. The polynucleotides may also be used to construct therapeutic purposes. The polynucleotides may also be used to construct two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
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                                                                                                                                                                                                                                                                The present invention describes a library of human polynucleotides
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                                                                    Novel human genes and their expression products which are differentially expressed in different cell types
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                                                                                                                                                                                        Claim 1; Page 1097; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and lung cancer. The polynucleotide peptide analogues and antagonists.
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ID AAF16372 standard; cDNA; 236 BP
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Matches 42; Conservative
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Rattus norvegicus tinman homolog (rNKx·2.º) mRNA, complete cds.
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Submitted (03JW-1997) Medicine, UCSD, 9500 Gilman Dr., La Jolla,
CA 9209:-6613, USA
Location/Qualifiers
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Mammalia; Eutheria: Rodentia: Sciuroqnathi: Muridae; Murinae;
                                                                                                                                                                                                 Cambridgeshire
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Vector are available from the HK MPC Human Genome Mapping Project Clones are available from the HK MPC Human Genome HK. See HRL: Resource Centre, Hinxton, Cambridgeshiro CPiù IRC, UK. See HRL: http://www.hmp.mrc.ac.uk/ for dotails or contact: blobabphmap.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                                               Direct Submission Submission Submitted (16-oct-1995) The Sanger Centre, Hinxton, Cambridgeshire CBIO 180, FORT-1995) The Sanger Centre, Humquery-sanger ac.uk CBIO 180, FORT-180, Submitted (16-oct-180, Submitted (18-oct-180, Submi
                         Homo sapiens
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
Mammalia: Luc 251)
MacDonald.M., Huckle,E., Wilkinsenn.P. and Micklem.G.
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/db_xref="taxon:10116"
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/db_xref="taxon:9656"
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/clone="94e8"
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Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Homo.
Topota,M., Ho,C., Ahuja,N., Jair,K.W., Li,Q., Ohe-Toyota,M.,
Baylin,S.B. and Issa,J.P.
Baylin,S.B. and Issa,J.P.
Identification of differentially methylated sequences in colorectal
cancer by methylated (PG island amplification
Cancer Res. 59 (10), 2307-2312 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human: immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ79353 shows the nt. sequence of the entire 9 a kb genemic clone happle. This nucleic acid sequence includes a coding sequence, a 5 flanking region contq. multiple restrictory elements and a 46 flanking region contq. multiple restrictory elements.
                                                                                                                                                                                                                                                                                                                                                                 New regulatory regions of human erythropoletis gene - used for studying and treating diseases and for produs of transgenic animal models.
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Best Local Similarity 100.0%; Fred. No. 6.2e-160
Matches 74; Conservative 0: Missarches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK87546 standard: DNA; 52:1 BP
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2000US-0189874.
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2000US-0205515.
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2000US-6216647.
                          94WO-0504141
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16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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04-FEB-2000;
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                                                                                       15-APR-1993;
23-JUN-1993;
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                                                                                                                                                                                                                                              Lee-huang S:
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                              15-APR-1994
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S
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                                                                                                                                                                                                                                                        AAU79353 shows the nt. sequence of the entire 9.3 kb genomic clone hebsil. This nucleic acid sequence includes a coding sequence, a 5' flanking region contg. multiple regulatory elements and a 3' flanking region contg. multiple regulatory elements. AAU79355 consists of the last 1777 bases of AAQ79753. It corresp. to the noncoding 3' flanking region of AAQ79753 and includes all the regulatory elements contained therein. It extends from the 5'-most pst1 site 3' of the end of the coding sequence to a BamHi site. It comprises 177 be exhibiting many stem-loop structures. It also contains TATA bases in forward and reverse orientation, and at least about 184 potential transcriptional regulatory elements. These elements include TRIID, metal responsive elements, glucorcorticoid responsive element (includer TRIID, metal responsive elements, glucorcorticoid responsive elements (including GR/PR-MMTV), NF-kappa-B, AF1, AF2, Sp1, and lymphoxima responsive consensus sequences, and many others. This region also contains two nitrogen regulatory/oxygen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4376 teceagetaetegggaaggetgaggeaggagaategettgaaceegggaggeggaggttge 4435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genomic clone hBpSLH including erythropoietin (BPO) coding sequence and 5' and 3' regulatory elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                   New regulatory regions of human erythropoietin gene · used for studying and treating diseases and for prodn. of transgenic animal models.
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Pred. No. 7.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.9%; Score 74; DB Best Local Similarity 100.0%; Pred. No. 7.2 Matches 74; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                         Claim 1; Page 57-58; 81pp; English.
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2304..2309
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                       WPI: 1994-141353/42.
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RESULT 13 AAQ79353/c

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7. Gaps

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Run on:

July 6. 2002, 20:18:21; Swarch time 239.41 Seconds (without alignments) 6926.493 Million cell updates/sec US-09-761-466-5 6751 lithe: Perfect score:

l caattictatinagiticiatadittaaaccogqqtfqfff 675] otiso_NUC Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

\$83533 seqs, 122816752 residues World size : Searched:

767056 Total number of hits satisfying chosen parameters:

Minimum DB seq leadth: 0 Maximum DB seq leagth: 200000000

Post processing: Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Mateb	Query Match Length DB	ΩB	ID	Description
-	4.1	0.0	308	. 2	US-08-721-488-4	Sequence 4, Appli
. 2	4	9.0	1134	رمی	US-09-248-345-29	Sequence 29, April
~	4]	9.0	1720	4	US-09-227-357-139	Sequence 139, App
.	4.1	0.6	2209	r	US-98-514-014-1	
u"	-	0.6	2209	~	US-98-833-823-1	
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17	: · •	11.6	515	4	US-08-785-271-1	Sequence 1, Appli
	4.0	0.6	630	-	US-08-185-414E-1	_
5 .	-) 4	9.0	190	7	US-09-461-474-13	_
. 20	4-0	9.11	806	4	US-38-955-6295-1	_
7.	4.0	9.0	857	-	US-98-308-883-1	_
77	7	9.10	857	-	US-48 740-164-1	-
+7	4 1/1	9.5	857	7	US-18-256-799-1	_
7.7	40	9.11	857	4	US)8-46.2-447-]	. =
57 .	4	9.7	1023	,4	US-08-252-906B-16	Sequence 16, April
37	7) *0*	9'	1066		US-J8-157-101A-4	• •
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2.6%; Street, No. 1.40. (1921) 12. (2. 1)

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# wa a a a a a a a a a a a a a a a a a a	RESULT 1 188-4/C Separate 4, Application US/08721488 Separate 4, Application US/08721488 Paton No. 595508 GENERAL INFORMATION: Renneth APPLICANT: MCCOp. John SECTION OF SEGUENCES: ALMERSEE: ACCOPATION OF SEGUENCES: ACC
१९०१६१२२५८८२२५५ प्राच्चव्यव्यव्यव्यव्यव्य	TO A SAME
발경수무한 CIP 등 등 등 중 중 중 글 글 글 글 글 돌 달 달	SULT 1989 SEQUENCY 1988 SEQUEN
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APPLICATION NUMBER: 60/052,733 FILING DATE: 1997-07-08

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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
                                                                                   EARLIER APPLICATION NUMBER: 60/052,795
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APPLICANT: WOGONIGLE, BRIAN
APPLICANT: O'REEF, DANIEL
JITUEO RY INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT APPLICATION NUMBER: 08/924,759
EARLIER PILICATION NUMBER: 08/924,759
EARLIER PILICATION NUMBER: 08/924,759
SOFTWARE: MICROSOft Word Version 7.0A
SOFTWARE: MICROSOft Word Version 7.0A
SOFTWARE: MICROSOft Word Version 7.0A
LENGTH: 1134
TYPE: DNA
ORGANISM: maize
US-09-248-335-29
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                                                     Score 41; DB 3; Lo
Pred. No. 1.3e-05;
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APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
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CORRENT AFFLICATION NUMBER: US/09/22/, 33/
EARLIER FILING DATE: 1999-01-08
EARLIER FILING DATE: 1999-07-07
EARLIER PPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER PLING DATE: 1997-07-08
EARLIER PPLING DATE: 1997-07-08
EARLIER PLING DATE: 1997-07-08
EARLIER PPLICATION NUMBER: 60/051,930
EARLIER PPLING DATE: 1997-07-08
EARLIER PLING DATE: 1997-07-08
     Mismatches
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                                                                                                                                                                                                                                       Sequence 29, Application US/09248335 Patent No. 6096504
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Best Local Similarity
                                                                                                                                                                                                                                                                Patent No. 6096504
GENERAL INFORMATION:
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41;
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100.0%; Pred. No. ...
0; Mismatches
EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,722

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,950

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,954

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,954

EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,661

EARLIER FILING DATE: 1997-09-12

EARLIER FILING DATE: 1997-09-12
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APPLICANT: MCCOY, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
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US-09-227-357-139
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APPLICANT: McCoy, John
APPLICANT: Mclefort, Kerry
APPLICANT: Vallebor, Kerry
FILE OF INVENTION: DNA SEQUENIES AND SECRETED PROTEINS
FILE OF INVENTION: ENGODED THEREBY
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STREET: 87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: The four in Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLING DATE: 10-APR-1997 CLASSIFICATION: 530
                                                                                                                                                                                SOFTWAKE: Patentin Rolease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514.914
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Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                       NAME: Brown, Scott A. Redistration NUMBER 12,724
REGISTRATION NUMBER 12,724
REDECOMUNICATION INFORMATION:
TELEPHYNE: (617) 498-8224
TELEFRY (617) 476-5851
INFORMATION FOR SECULO NO. 1:
SEGGENIE CHARACTERISTICS:
                                                                                                                      MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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: 47 CambridgePark Drive
Cambridge
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Fatent No. 5965093
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                       Allorney/AGENT INFORMATION:
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SIRANDEDNESS: double
                                        SIAIE: Massachusetts
                                                                                                  MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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MEDIUM TYDE: Fig.py disk
COMPUTER: TWN FC COMPATIBLE:
CPERTITUS SYSTEM: FOTOWSYMSTON FOTOWSYMSTON:
SUFTAME: Pat contin Release #i.e. Version #1.49
CURRENT APPLICATION DAIA:
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Bost Local Similarity Tollow: Prot. N. 1.2.
Matches 41: Conservative () M.Shar Ses
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APPLICANT: Liu, Yong Jun
APPLICANT: Liu, Ju
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STREED: 901 California Ascono
STREE: 910 California
STATE: Galifornia
                                                                                                                                                                                                                                                               | NAME: HOWE, SCOTT A. |
| FEGISTRAIL'O'N UNBER: 4.2.2.44 |
| FEFERENCE/FOOTKET UNBER: 016000
| TELEPHONE: (6.17) 4.98-42.44 |
| TELEPHONE: (6.17) 4.98-42.44 |
| TELEPHONE: (6.17) 4.98-42.44 |
| TELEPHONE: (6.17) 4.98-42.45 |
| TELEPHONE: (6.17) 4.98-42.45 |
| TELEPHONE: (6.17) 4.98-42.45 |
| TERGINE: 2.09 5.08.65 |
| TENGTH: 2.09 5.08.65 |
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68/514,114
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Futent No. Gu63229
GENERAL INFORMATION:
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TELECOMMUNISATION INPORMATION:
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                                                                                 FILING DAIB: 11-AGE-1995
ATIORNEY/AGENT INFORMATION:
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NAME: China, Edaito F.
RESISTRATT N NUMBER: 44.0
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          APPLICATION NUMBER:
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FILING DATE: U7-MAR
CLASSIFICATION: 530
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MOLECULE TYPE: CONA
HYPOTHELICAL: NO
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ZIP: 94 ked-11
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Self-ter

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Gaps

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Length 5962;

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GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Renener, Robert
TITLE OF INFORMION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 3
                                                                                         APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL, M.; CAMPBELL, KEVIN P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Score 41; DB 6; Length 596 Best Local Similarity 100.0%; Pred. No. 1e-05; Matches 41; Conservative 0; Mismatches 0; Indels
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STREET: 1660 Union Street
CITY: San Diego
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APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seidman, Stephanie L
REGIETRATION NUMBER: 33,779-53192
REFERENCE/DOCKET NUMBER: 6362-53192
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: LASTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastERO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,354B
FILING DATE: 15-FEB-1995
                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/482,384
FILING DATE: 20-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08404354B Patent No. 5618720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Ma
                                                                                                                                                    NUMBER OF SEQUENCES:
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                                   RESULT 8
5386025-5/c
;Patent No. 5386025
                                                                                                                                                                                                                                             ; LENGTH: 5962
5386025-5
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STATE: CA
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                                                                                                                                                                        Length 2280;
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                                                                                                                                                                                                          0; Indels
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100.0%; Pred. No. 1.2e-05;
iive 0; Mismatches 0;
                                                                                                                                                                    Query Match 0.6%; Score 41; DB 3; I Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 41; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Yue, Henry
TITLE OF INVENTION: CAFI-RELATED PROTEIN
WOMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0476 US
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REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                          US-09-027-137-2/c
; Sequence 2. Application US/09027137
; Patent No. 6013450
; GENERAL INFORMATION:
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COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 41; Conservative
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STRANDEDNESS: single
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; CLONE: 2229466
US-09-027-137-2
                                                                                             61..1470
                                   MOLECULE TYPE: CDNA
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                                                                           NAME/KEY:
                                                                                             ; LOCATION:
US-08-813-150-1
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CITY: Pal
STATE: CA
                                                         FEATURE
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APPLICANT: Elliss Steven Bradloy
APPLICANT: Blims, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Hermer Robert
ITLE OF INVENTIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bosty Match 0.6%; Score 41: DB 1; Longth 5975; Bost Local Similarity 100.0%; Pred. No. 1e-05: Matches 41: conservative 0: Mismatches 0: Indels
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STREET: 1640 Onion Street,
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SOFTWARE: PASISED VERSION 1.5
SOFTWARE: PASISED VERSION 1.5
CURRENT APPLICATION DATA:
PULING IARE: 28 SEEPT-1994
CLASSIFICATION: 435
PUCA APPLICATION: A75
PUCATION IARE: B 307/914.231
PULNG IARE: 1 34.07L-1992
PULNG IARE: 1 3.07L-1993
PULNG IARE: 1 3.07L-1993
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PEGISIPATI N NUMBER: 84,779
FECEPENCAZOVENI NUMBER: 642-53191
FELEPHONE: 419-238-1099
IELEFHONE: 419-238-1099
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Patent No. 5586241
                                                                                                                                                                                NAMEZKEY: Coding Sequence
CoCATION: 79...5700
CHER INF RMATION:
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FOOSTION: 79...5700
OTHER INPRAMATION:
GS-04-314-0844-1
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IBM Compatible
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FILING DATE: 08-NOV-1950
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
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LYPE: nacjeje acid
STRANJHJAESS: single
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CORRESPONDENCE ADDRESS:
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MEDIUM IYPE: Diskett
                                             TOPTION: Tinear MOLECULE TYPE: CDNA
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Malecule IYPE: cona
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STRANDEDNESS:
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COUNTRY: ....
9210]-
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US+08+414+084H+174
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                                                                                                                                                                                                                                                                                                                         US-04-404-3548-1
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APPLICANT: WIlliams, Mark F.
APPLICANT: Harpoid, Michael Mille;
APPLICANT: STORMERT Annold
APPLICANT: STORMERT Annold
APPLICANT: STORMERT AND METHODS
NUMBER F. SEQUENTS: G.
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200,0%; Prod. No. 4--57;
5co. 6; Missadottos
Sec. 1.55.
                                      5. 1.1.
                                                                                           Owery Match
Pest Loral Similarity Loryk: Prof. No. 16-55,
Matches 41: Conservation to Missishes
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Prown Martin, Hallor w Morlain,
SIREET: 1660 Daton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seidman, Stephanie I.
ENJISTRATION NUMBER: 44,779
REFERENCE/DOCKET NUMBER: (462-54)34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-FTWAKE: FASISED Version 1.5
POTERTH APPLICATION IN TAXAS
ARELICATION UNBER: USAN X/A KT.FTCB.
FILLING DATE: US-MAY-1.455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGURE PLANTION: "PRIOR PROBLEM APPLICATION NUMBER: US 08/414, CHA PILLING DATE: ZR-SEP-1944 FILLING DATE: ZR-SEP-1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-1992
MREE: US v7/65.,751
                                                                                                                                                                                                       Sequence 1, Application USZ 8435675F Patent No. 571025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERNATION FOR SECTION OF INSERTING SECURATE CHARACTER STITS:
LENGIH: $575 base pairs
TYPE: nucleir acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | NAME/KEY: Todino Sequence
| POATION 79, 1,57 |
| THER INFORMITON:
| USE 44 + 45 - 57 EE - 1
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COMPULER: IRM Compatible
(PERATING SYSIEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING BATE: OB-NOV-1999
ATTOKNEY/AGENT INF-RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rest Local Similarity 100.7
Matches 41; Conservative
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APPLICATION NUMBER:
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SIALE: CA
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                                                                                                                                                                      RESULT 11
US-08-435-6758-1/c
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TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
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COTHER INFORMATION: US-08-884-599-1
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                                                                                 San Diego
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                                                                                                       STATE: C. COUNTRY:
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LENGTH: 467
                                                            STREET:
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CCGATION: 79...5700
OTHER INFORMATION: \product- "Alpha-1 subunit of animal calcium
OTHER INFORMATION: channel"
                                                                                                 US-08-335-257A-3/C

Sequence 3, Application US/08336257A

Sequence 3, Application US/08336257A

Sequence 3, Application US/08336257A

Sequence 3, Application US/08336257A

Sequence 3, Application:

APPLICANT: Jay, Scott D

APPLICANT: Harpold, Michael M.

APPLICANT: Campbell, Kevin P.

TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA
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Patent No. 6013474
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Williams, Mark E.
APPLICANT: GENERAL SCHWARTE.
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL, COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6%; Score 41; DB 1; Length 5975; Best Local Similarity 100.0%; Pred. No. 1e-05; Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
OPERATING SYSTEM:
SOSTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,257A
FILING DATE: 07-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L.
REGISTRATION NUMBER: 54898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0962
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                             STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUWTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA
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NGS-08-841-349-18
Sequence 18, Application US/08841349B
Sequence 18, Application US/08841349B
Patent NO. 5955594
GENERAL INFORMATION:
APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENERAL OS OS INVENTION: GENERAL US/08/841,349B
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT PILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 1e-05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6362-53191B
                                                                                                                                                                                                                                               OFERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,599
FILING DATE: 27-UNE-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
PRIOR APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 79...5700
                                                                 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.6*
Best Local Similarity 100.0
Matches 41; Conservative
                                                                                                                                     COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-238-0062
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EDNESS: single
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: FIRER INPORMATION: For all n's in this sequence, n-(a or q or c gr t) US 08-841-349-18
                                                                                                                                                                                                                                                TACKIN NO. 128.

FARLICANI: NO-WAGATG. Christopher B. APPLICANI: NO-WAGATG. Christopher B. APPLICANI: No-Wagard. Philippe
APPLICANI: Mabban, Philippe
APPLICANI: Glark, Samuel A. APPLICANI: Glark, Samuel A. APPLICANI: Quade, Christian
APPLICANI: Quade, Christian
APPLICANI: Quade, Christian
APPLICANI: Glark, Secretory Gell Lines
ITILE OF INVENTION: Secretory Gell Lines
NUMBER OF SEAPTHORES: Secretory Gell Lines
CURRESPONDENTE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOODTY Match 0.6%; Secret 40: DB c; Length 515; Best Local Similarity 100.0%; Pred. No. 3.3e-05; Marches 40; Conservative 0; Mismatches 0: Indels
                                                            Length 467;
                                                                                       U: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 6.6%; Score 46; ER 2; LK Best Local Similarity 160.6%; Fred. No. 3.4e-05; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: July 6, 2002, 20:20:11 Job time: 54296 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                                                                         Sequence 1, Appileation US/08589028
Patent, No. 6887129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : TOPOLOGY: linear
US-08-589-028-1
                                                                                                                                                                                          RESULT 15
US 68-589-028-170
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us-09-761-466-5.rst

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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oM nichele - nucleic search, using sw model

July 6, 2002, 15:24:07 ; Search time 10026.1 Seconds (without alignments) 9088.102 Million cell apdates/sec Run on:

US-09-761-466-5 6751 | caalilglatinadilotat.....aqillaaaceqqqilditt 6751 Title: Periect score:

Scoring table:

sequence:

Gapop 60.0 , Gapext 60.0

Word size :

1.736207 seqs, 6748477542 residues

Searched:

274724:4 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

*:188 Database :

| ... em_estba;*
| ... em_estbun;*
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| ... em_estov;*
| ... em_estov;*
| ... em_estov;*
| ... em_esto;*
| ... em_esto;*
| ... em_esto;*
| ... em_sspil;*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	± 3	Score		Chery Match Length DB	<u>*</u>	ID	loseription
c	-	475	7.0	815	حر.	A1609745	A1609745 t182401.x
U	~	456	4.5	713	2	AW665197	AW665197 hj91q01.x
U	~	443	6.6	2.40	*	A14788 + 9	A1478839 tmz4eJ4.x
O	4	4 38	4.5	674	£	A1936496	AI935496 wd28104.x
	un.	425	6.3	457	5	AW001138	AW001138 w124407.x
ن	٩	408	6.0	542	Ţ	AU145160	AU146160 AU146160
	7	406	6.0	206	Ĵ	AU1:9953	AU119953 AU119953
Ü	œ	568	5.9	418	٠,	AI347524	A1347523 4492a02.x
	5	3.93	80.	908	-	B1844117	BIB34117 FF4085284
t	0:	345	£.	546	œ	AA7.22525	AA722525 7480ev7.s
		*16	4.7	628	0.1	BF:15950	BF115950 7n75b04.x
ن	1.7	\$12	4.6	4.21	î,	A1424518	A1424518 t162d04.x
C)	-	309	4.6	555	10	BF510466	BF510466 UI-H-B14-
	14	277	4.1	360	12	A0883290	AQ883250 HS_5465, E
	u"	270	4.0	638		BG:15100	MG115100 602415938
	Ę.	197	2.2	763	\Box	BIR35590	M1835590 6030088944
	17	205	4.0	1587	01	BM470688	HM470688 AMENCOURT

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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:2980560"
/clone="IMAGE:2980560"
/clone=lib="Scares_WFL_T_GBC_SI"
/lab.host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (fetal lung NHL19W, testis NHT, and B-cell libraries (fetal lung NHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480:030287, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soarce and M. Fatima Bonaldo.
                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttgtggcgcgattatgcagcgtgcaatgagtgatcctgcagcctggtgtcttagctgtc 5685
                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 466.
Location/Qualifiers
1.713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccactgccgccgccaacaactacttcgtgaacttcggcgtcggggacttgaatgcggttc 5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctgcggagacctaggaactttttctgtcccacgcgcgtttgttcttgcgcacgggaggt 5625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 CCACTGCCGCCGACCAACAACTTCGTGAACTTCGGCGTCGGGGACTTGAATGCGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 9;
4.6e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 466;
Pred. No. 4
                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%;
Best Local Similarity 99.6%;
Matches 566; Conservative (
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                                               Tumor Gene Index
Unpublished (1997)
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IMAGE:2980560 3' similar to SW:HK25_HUMAN P52952 HOMEOBOX PROTEIN
KXX-2.5; contains Alu repetitive element;, mRNA sequence.
AW651197. GI:7457743
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 /tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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/note—Totan: pooled: Vector: p17T3D-Pac (Pharmacia) with a modified polyplinker: Site_1: Not 1: Site_2: Eco KI: Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and H-cell libraries (fetal lung NBHL19W, testis NHT, and H-cell vito. Gollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clouds made from the same 3 libraries. The pools consisted of 1.M.A.C.E. clones 297480-392808, 682632-687239, 72408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 2 others
                                                                                                                                                                       A1478839 590 bp mkNA linear ESI 14-APR-1999 tm24c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157534 3' Similar to TR:P97335 P97335 HOMEOBOX. ;contains A1478839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-rāmail.nih.gov
This clone is available royalty-free through LLNL: contact the
TMAGE Consortium (into image.llnl.gov) for further information.
Insert Length: 1845 Std Error: 0.00
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref-"taxon:9606"
/clone="IMAGE:2157534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
5865 ctytaayaaatqacqatcccctt.cccat, 5893
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High quality sequence stop: 464.
                        44 CIGIAAGAAAIGAGGAICCCTICCCAT 17
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Addition="Homo sapiens"

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##ZES104.x1 Soares_NFL_T_GBC_S1 Home Saprons close
IMAGE:2329471 3' Similar to SW:HKZ5_HEMAN P5Z35Z HOMEOBOX PFGTEIN
NX-2.5 : MRNA Sequence.
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1 (bases 1 to 674)
NOI-GGAP http://www.ncbi.nlm.nlm.gox/nch.rag.
NoI-GGAP http://www.ncbi.nlm.nlm.gox/nch.rag.
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This clone is available royalty-tree through LLNL r contact the This clone is available royalty-tree through LLNL r contact the Mande Consortium (into dimage.llb.dov) For Purther information. Hande Consortium (into dimage.llb.dov)
Seq primer: -400p from Othero
High quality sequence stop: 452.
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5717 caccecedatidaaantaquantaayeteydaeeaenakkakentaaqatetaaeegeea 1774
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Pred. No. 1.40-76.
0: Mismarches +: Indels
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/db_xref="taxon:9606"
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/clone=lib="scares_Dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.).
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/lab_host="DH10B (phage-resistant)"
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HRI Juman chwa project (eta.T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamofo,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Maqai,T., Suqano,S., Isoqai,T.)
Uppulishq (200)
                                                                                                                                                                                                                                                                                                                         Email: qenomics³hrl.co.jp
Hrl human cuNA project; 5. & 1'-end one pass sequencing: Hellx
Pessarch institute; cNW, library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
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/dov_stage="embryo, up weeks"
/note="vector: pME188F13" 7 other
157 c 164 q 97 t 7 other
                                                                                                                                                   Genomics Laboratory
Hellx Research Institute
1823-Y Yaha, Kisaratu, Chiba 292-0812, Japan
16:: 8-478-52-8951
Fax: 81-438-52-8952
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/clone="HEMBA1007016"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares
                                                                                                                                             Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 418)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 606 Std Error: 0.00
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Preparation: Life Technologies, Inc.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11564 row: g column: 22
High quality sequence stop: 736.
I. Sequence stop: 736.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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40 GAAATGACGATCCCCTTCCCATTAAAGAGAGTGCGTTGA
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/clone_lib="NIH_MGC_120"
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Hiller, A. Allen, Mewles, L., Dubuque, L., Geisel, G., Jost, S., Krizman, D., Kuraba, F., Tary, M., Le, N., Lennon, G., Marra, M., Martin, M., Moore, B., Schellerhera, K., Steptoe, M., Tan, F., Theisina, B., Wastin, Y., Wile, T., Waturston, R. and Wilson, R.
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Z4B0007.s1 Soares_fetal_heart_NbHH19W Homo sapieus chun clone
IMAGE399684 f similar to SW:HK25_HUMAN P52952 HOMEORUX PROTEIN
NKX.2.5 ; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMACH Consortium (info*image.llnl.dov) for further information. Dossible reversed clone: similarity on wrons strand. Seq primer: *40m13 Lwd. ET from Amersham High quality sequence stop: 202.
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Best Local Similarity 100.0%; Pred. No. 24-58;
Marches 345; Conservative 0: Mismatches 0; Indels
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Fax: 414 286 1810
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Tissue trochicument Christopher A. Moska, dk. M.D., Ph.D., Michael
E. Burert Fock, M.D., Ph.L. 97NA Illiany freperation: M. Bento
Soares, Ph.D. eDNA Library Arrayor (p. Phr.St. France, Ib-
I.M.A.G. E. Consort for INA Sequencina by Washington University
Genome Sequencina Center
Clone distribution: Net-confer exort Service distribution intermation can be
found through the I.M.A.G.E. Kansert Epylink, send email for
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Mammalia: Butherba; Primates: Catarrin; Hominidae: Homo.
1. (bases: 1 to A2M)
NCI-CGAP http://www.nebi.nlm.mil.non/uciedap.
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DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 156 Std Error: 0.00
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                             4862 cgcggagcggccccgggcgcgacggcggaggaagccgcgcgcgtgctcttctcgcaggcgca 4921
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                                                        Length 628;
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                                                      Score 316; DB 10;
Pred. No. 7.2e-53;
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 86
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/db_xref="taxon:9606"
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Location/Qualifiers
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AI424518.1 GI:4270449
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Best Local S
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BASE COUNT
ORIGIN
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:

I.M.A.G.E. Consortium/ILNL at:
Seq primer: M13 Forward
                                                                        BF510466
UI-H-BI4-aoe-h-03-0-UI.sl NCL_CGAP_Sub8 Homo sapiens cDNA clone
IMAGE:3084892 3', mRNA sequence.
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1 (bases 1 to 555)

10 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                3 others
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          /clone_lib="NCI_CGAP_Brn23"
/tissue_type="qlioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                               Score 312; DB 9;
Pred. No. 7e-52;
                                                                                                                                                                                                                                                                                                                                / Match 4.6%; Score 312; UB Local Similarity 100.0%; Pred. No. 7e-
/clone="IMAGE:2103847"
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BF510466.1 GI:11593764
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/ub_xrel="laxon:9466"
/ub_xrel="laxon:9466"
/clone="lhadb:30b48"
/clone="lhadb:30b48"
/clone="lhadb:30b48"
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/clone="laxon:94666"
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Prod. No. 1.9e-51;
G: Mismatches 0; Indels
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Best Local Similarity 99.8%:
Matches 429: Conservative 6
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Contact: Mahairas GD, Wallage JT, Baod I
High Throughput Sequencina Contact
University of Washington
And Queen Anno Accord Morth. Seattle, WA 98134. SSA
fel: (2003) FF GF8
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Male blood LNA was isolated then see landomly chosen deformand pathodly digested with a sembination of EcckB and Pertha Melhylase. Size selected that was cloned into the pEAGE-3 words at EcckB SLPes. Collects.
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3.1. Year L. Chaq, S., Adams.M.P.
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Mahairas, S.R., Walface, J.S., Sc
Keller, A., Shaker, E., Firlian,
Hood, L.
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E. I (bases 1 to 938)

S. NIH-MGC http://mgc.nci.nih.gov/

I. Onpublished (1999)

L. Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAL at:

http://image.llnl.gov

Plate: LLAM10147 row: k column: 09

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/db_xref="taxon:9606"
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/clone="INAGE:4416518"
/clone_lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_host="5DHOB (phage-resistant):
/note="0rgan: small intestine; Vector: pCWV-SPORT6;
Site_l: Not!; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
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Technologies. Note: this is a NIH_MGC Library."
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HTG 18-JAN-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 134624 bases at least 040
Consensus quality: 135712 bases at least 030
Consensus quality: 135772 bases at least 020
Insert size: 136057; sum-of-contigs
Insert size: 115180; 6.1% error; agarose-fp
Quality coverage: 7.81x in 020 bases; sum-of-contigs Quality
coverage: 9.23x in 020 bases; agarose-fp
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                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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ALDUNY24
Homo sapiens chromosome 6 clone XXbac-250J14,
PROGRESS ***, 7 unordered pieces.
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Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens'/db_xref="taxon:9606"
/chromosome="6"
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sum-of-contigs Quality

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Db 11094 AGAGAAAICATTACCGGATICACAAAGGCATAGAGAGTGTAACAGTCACTGATCTTGTT 11153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * arbitrary, Gaps between the contins are represented as * runs of N. but the exact sizes of the daps are unknown. This record will be updated with the linished sequence as soon as it is available and the acression number will * be preserved.
             On Jan 15, 2002 this sequence version replaced all 18152648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequency, it currently 
* consists of 4 contigs. The trae order of the pieces 
* is not known and their order in this sequence record is
                                                                                                                                                                                                   Assembly program: NAAP4: vorsion 4.5
Sequencing vector: plasmid: 104952; 150% of reads
Sequencing vector: plasmid: 104952; 150% of reads
Chemistry: Dye-terminator bid 1995; 160% of reads
Consensus quality: 14472 bases at least 040
Consensus quality: 14422 bases at least 040
Consensus quality: 14422 bases at least 020
Lisert size: 144429; same-of-configs
Lisert size: 16969: 14 % 0100; adapted: [0.00]
Quality coverage: 16,72x in Q2v bases: sum-of-contias
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76929 116346; contid of 45878 bp in length
11647 116445; aap ol len hp
116447 131258; contid of 18482 up in centh
131259 131358; qap of length pp in length.
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99.8%; Pred. No. 1.se-199;
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coverage: 9.55x in 620 bases: adamose-1p
                                                       Center: Wellcome Trust Sanger Institute
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framment_chain:1
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fragment_chain::"
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                                                                                                                                                         Project Information
                                                                                                         Web site: http://www.sanger.ac.uk
Contact: humquery sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sap.ens"
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Zelone_11be "CBpk:-5-1
                                                                                                                                                                                   Center project name: bPG116A1
                                    Genome Center
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ORIGIN
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             COMMENT
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Homo sapiens chromosome 5 clone XXbac-116Al, *** SEQUENCING IN
PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity 99.8%; Pred. No. 1.3e-195;
Matches 477; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                    601 others
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47616. 52829
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52930. 90493
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5, 2002, 10:27:10 Search completed: July Job time: 6432 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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5, 2002, 09:25:58; search time 210.97 Seconds (without alignments) 3850.056 Million cell updates/sec
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US-09-761-466-6
478
Title:
Perfect score:
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l agagaaatcattacccgutt......ggcatcctccaacqacac 478 Sequence:

1736436 seqs, 858457221 residues Searched:

Gapop 60.0 , Gapext 60.0

OLIGO NUC

Scoring table:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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/SIDS1/gcgdata/hold-geneseq/qeneseqn-embl/NA2002.bai:+ Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	DNA encoding hcsx/ Genomic DNA #2 enc
15	478 22 AAS09963 6751 22 AAS09962
DB	22
ength	478
Query Score Match Length DB ID	478 100.0 478 100.0
Score	1 478 100.0 478 22 AASO 2 478 100.0 5751 22 AASO
Result No.	1 5

ALIGNMENIS

RESULI 1 AAS09953

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of cardiomyocyte induction, e.g. for optimistrat cardiomyocyte induction. Genes expressed in the cardiac cell-special minion are useful for the targeted expression of genes encoding the appeal of the treatment of damaged heart tissue. Cardiac specific enhancer elements may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents the coding sequence of vardiac enhancer hCsx/Nkx2.5 homology domain B. The northern acts is useful for specifically expressing a gene in a curnar cell, as an earlier marker
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therapeutic: wart tissue; dene therapy; biman, ds.
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                                                                                          NNA encoding 1/3x/Nkx2.5 homology domain B.
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ilarity 100.0%; E
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AAS09967 standard; DNA; 478
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                                                              (first entry)
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Best Local Similarity
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                                                                                                                                                                       Homo sapiens.
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SUMMARIES

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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_htgo_inv:*
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Maximum Match 100%
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Maximum DB
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                                                                                                                                                  Summary Statistics
Consensus quality: 123959 bases at least 040
Consensus quality: 13398 bases at least 030
Consensus quality: 134736 bases at least 020
Consensus quality: 134736 bases at least 020
Estimated insert size: 135340; agarose-fp estimation
Estimated insert size: 135595; sum-of-contigs estimation
Quality coverage: 4.91 in 020 bases; sum-of-contigs estimation
Quality coverage: 4.91 in 020 bases; sum-of-contigs estimation
* ronsists of 21 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                        the accession number will be preserved.

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 162: contig of 162 bp in length 2163: contig of 162 bp in length 5224 5323: gap of unknown length 5324 5323: gap of unknown length 5324 15199: contig of 9876 bp in length 15200 15299: gap of unknown length 15300 22312: contig of 9876 bp in length 22313: 22413: 37107: contig of 14695 bp in length 37208 37207: gap of unknown length 37208 43864 43963: contig of 6656 bp in length 43964 46965: contig of 6656 bp in length 43964 46965: contig of 3002 bp in length 45966: contig of 3002 bp in length 45966: sontig of 13002 bp in length 45968: contig of 4406 bp in length 45978: gap of unknown length 49478 49578: contig of 2412 bp in length 49578: 54524: 56532: contig of 496 bp in length 54523: contig of 4946 bp in length 54524: 56532: contig of 496 bp in length 55524.
                                                                                                                                                                                                                                                                                                                                                                      * is believed to be correct as given, however the sizes to the gaps between them are based on estimates that have * provided by the submittor.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length contig of 13791 bp in length gap of unknown length contig of 4336 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 10225 bp in length contig of 10225 bp in length
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gap of unknown length
contig of 9136 bp in length
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f unknown length
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/clone="CTC-281H14"
/clone_lib="CalTech human BAC library C"
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of 7271 bp in length
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of 3307 bp in length
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134038: contig of 3815 bp in length
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136470: contig of 2332 bp in length
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137545: contig of 975 bp in length.
                                                                                                                    Center clone name: CIT-HSPC_281H14
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                        Web site: http://www.jgi.doe.gov
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118552: contig of
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128298: gap of unk
130123: contig of
Center: Joint Genome Institute
Center Code: JGI
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FEATURES SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, Callo 15A, UK. E-mail enquiries: humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk on Jan 25, 2002 this sequence version replaced gi:18250865.
                                                                                                                                                                                                                                                                                                                36587 CAAATAGGGAGAGTTTTTTTTCCTTCCCTTTTTGTAACACCTGACCCACAGGACTGACAG 36646
                                                                                                                                                                                                                                                                                                                                                                                   36527 AGAGAAATCATTACCCGATTCACAAAGAGCATAGAGAGTGTAACAGTCACTGATCTTGTT 36586
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Homo sapiens chromosome 6 clone XXbac-250J14, *** SEQUENCING IN
PROGRESS ***, 7 unordered pieces.
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                                                                                     Length 137545,
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  2000 others
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Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 134624 bases at least Q40
Consensus quality: 135417 bases at least Q30
Consensus quality: 135772 bases at least Q20
                                                                                     Score 476.4; DB 2;
Pred. No. 1.1e-120;
0; Mismatches 1;
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Direct Submission
                                                                                                            Similarity
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Mon Jul

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CB 46484 AGAGAAATCATIACCCGATICACAAAGAGCAAAAGAGTGTAACAGTCATCTTSTT 46424
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Insert size: 146-57; sum-of-conflus
insert size: 117140.5 AB error; adarose-Ip
exally coverage: 2.81x in Q20 bases: sum-of-conflus oddity
exercise: 9.2xx in Q20 bases; adarose-Ip
                                                                                                       • NoTE: This is a 'working draft' sequence. If currently evansists of 7 conties. The true order of the pieces is not known and their order in this sequence record is units of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as all is available and the accession number will be preserved.
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99.6%; Pred. No. 8.2e-118;
ive 0; Mismatches 0; Indels 1;
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7624 41860: contig of 3437 bp in length
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/rote-"assembly_fragment:01480
franment_chain:1
coloue-end:17
vertor_side:1eft."
7524. 41 %0
fragment_chain:1
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47616. 52829
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foote "assembly_fragment:00959

tradment_chain:1"

90594. ...109605

//note-"assembly_tradment:01522

fragment_chain:1"
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/note="assembly_fragment:02092
fragment_chain:1"
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/db_xref:"taxon:9606"
/chromosome="6"
/elone "Xxbag-250J14"
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1. .136657
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136657: conti
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Best, Local Similarity 99.8%
Matches 477; conservative
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109906 13665
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1 (bases 1 to 8117)
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                                                                                                                                                                      Searcy, R.D., Vincent, E.B., Liberatore, C.M. and Yutzey, K.E. AGATA-dependent inx-2.5 regulatory element activates early gene expression in transgenic mice
Development 125 (22), 4461-4470 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-SEP-1998) Molecular Cardiovascular Biology, Children's Hospital Research Foundation, 3333 Burnet Avenue, Cincinnati, OH 45229, USA
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/gene="Nkx-2.5"
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REFERENCE AVIBORS TITLE JOURNAL AUTHORS AUTHORS TITLE AUTHORS	Mammalia: Eutheria: Rodeutia: Schurodnath: Muridae, Muricae: Mis. [(bases 1 to 21918)] Martin, J. Hosseini, K., Penq, Y., Penq, Z., Rubin, E.M. and Theng, J.F. Direct Submission Unpublished 2 (bases 1 to 219180) Martin, J. Hosseini, R., Penq, Y., Penq, Z., Chenq, JF.F. and Rubin, E.M. Fulli, J. Hosseini, R., Penq, Y., Penq, Z., Chenq, JF.F. and Fulli, J. Hosseini, R., Penq, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Y., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, J. Hosseini, R., Peng, Z., Cheng, JF.F. and Fulli, R., F., F., F., F., F., F., F., F., F., F
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B4133
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AUTHORS
111.E
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Submitted (21-NoV-2001) Wellcome Trust Sanger Institute, Hinxton, cambridgeshlre, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 25, 2001 this sequence version replaced gi:17043820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 2 clone RP11-404F23 map 2, SCOURCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; 108752; 100% of reads Sequencing vector: plasmid; 108752; 100% of reads Chemistry: Dye-terminator Big Dye; 99% of reads Chemistry: Dye-primer Big Dye; 0% of reads Consensus quality: 191473 bases at least 040 consensus quality: 191494 bases at least 030 consensus quality: 191494 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:03311"
46072 c 46038 g 49696 t
                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44.2;
Pred. No. 0.3
                                                                                                                                                                                                                           Center project name: bM36P22
                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                     ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP23-36P22"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                 -- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                 Pearce, A.
Direct Submission
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HTG; HTGS_PHASE0
                                                                                                                                                                         Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
 (sites)
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ORIGIN
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                                   TITLE
JOURNAL
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               AUTHORS
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KEYWORDS
SOURCE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                             COMMENT
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                                                                                                                                                                                                                                                                 /translation="MFPSPALTPTPFSVKDILNLEQQQRSLASGDLSARLEATLAPAS
CMLAAFKPEAXSGPEAAASGLAELREMGPAPSPPKGSPAPFPAAPTFYPGAYGDPDPA
KDPRADKKELCALQKAVELDKAETDGAEPPRARRRKPRVLFSQAQYYELERRFKQR
YLSPAERDQLASVLKLTSTQVW. THEONRRYKCKRQRQDQTLELLGPPPPPARRIAVPY
LVRDGKPCLGDPAAYAPAYGVGLNAYGYNAYPPSYGGAACSPGYSCAAYPAAPAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus chromosome 2 clone RP23-36P22, *** SEQUENCING IN PROSRESS ***, in ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3346 TCAGCAAGACATTTAATTGAATCGGATGTGGCTCGTTTGCCAGACGTCACCGCCTGGGTG 3405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3009 GGGTGGGAAAGTCACTGATTTGTTCAAATTAGAAGAGTTTT-----CTTCCTTTTTTTTT 3063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3172 TITIAAAAAAGACTIAAAACAGGGATCCCGGATGGGGGCCCCCAAIAITGCTC-----CC 3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3122 AAICCTCACCACATIGATITGCAAAGGAAACG------TCCCCTCTCAAAACIAIT 3171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 aacacctgacccacaggactgacagttctaggaagcccccttacccgaaaataggaaata 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 agccgcctggccagcagattcacttaacagcgctcccaggaccctcgttccgagctcttt 395
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AL591488.7 GI:17065727
HTG: HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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     /product="cardiac homeobox transcription factor"
join(5100. .5734,7132. .8114)
/gene="Nkx2-5"
                                                                                   /product="cardiac homeobox transcription factor"
join(5424. .5734,7132. .7757)
/gene="Nkx2-5"
                                                                                                                                                                                                         /product="cardiac homeobox transcription factor"
/protein_id="AAG38875.1"
/db_xref="GI:11602838"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                              APAASANSNFVNFGVGDLNTVQSPGMPQGNSGVSTLHGIRAW"
2336 c 2179 g 2091 t 1 others
                                                                                                                                               /function="involved in heart development"/note="tinman homolog; Nkx family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 182.2; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.4e-39;
/note="alternatively spliced"
                                                                     /note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                              2179 g
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71.6%;
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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HTG 28-MAR-2000
LOW-PASS
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 tcaaaaaaaaaaaaaaaaaaaacettactaaaaaacagggatcccggatgtagcctcgatgt 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 191494; sum-of-contigs
Insert size: 168060; 8.7% error; agarose-fp
Quality coverage: 16.18x in Q20 bases; sum-of-contigs Quality
coverage: 18.44x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                     * This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 191494;
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9940 10039; cap of 1003 ft in the 10040 10039; cap of 10040 10037; cap of 10040 10034; cap of 10040 11569 12594 12591; cap of 10040 11569 11569 11569; cap of 10040 11563 1406; cap of 10040 11563 11660; cap of 10040 11563 11660; cap of 10040 11563 11660; cap of 10040 11604; cap of 10040	21944: 934: 00114 0.9 19 19 19 19 2275: contiq cd 75 h in 2345: uap of 10 h by 2345: qap of 10 h by 2441: contiq cd 75 h in 2454: qap of 10 h by 2547: contiq cd 824 h in 2657: contiq cd 826 h in 2657: qap of 10 h by 27287: qap of 27287: q	291.7: qup vol.1 a 292.07: qup vol.1 a 292.07: qup vol.1 a 292.07: qup vol.1 a 30.966: rontid a 30.966: rontid a 318.2: rontid a 372: qup vol.1 a 428.2: rontid a 458.2: rontid a 458.2: rontid a 458.2: rontid a 458.2: qup vol.1 a 458.2: rontid a 458.2: rontid a 458.2: qup vol.1 a 460.5: contid a 410.2: contid a 410.2: contid a 410.2: contid a 410.2: qup vol.1 a 410.2: contid a 410.2: qup vol.1 a 428.2: rontid a 420.3: qup vol.1 a 428.2: rontid
He is (bases 1 to 72481) Shirten, H. Linton, L., Nushaum, C. and Lander, E. Thom saples chromosome 2. clour RPII-404F23 Unpublished E 2 (bases 1 to 77483) Shirten, L. Linton, L., Nushaum, C., Lander, E., Abraham, H., Ailen, N., Adderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boduslarkly, L., Foukhgalter, B., Brown, A., Burkett, G., Collymere, A., Cooke, P., Daver, R., Diaz, J.S., Collymere, A., Cooke, P., Daver, B., Etrihuth, W., Gallann, L., Gallaunn, J., Gardyna, S., Sinde, S., Goyette, M., Graham, L., Grand-Fierre, N., Graham, E., Johnson, R., Johnson, E., Helin, J., Lakocque, K., Lamazares, R., Landers, F., Lehotok, J., Klein, J., Lakocque, C., Lian, J., Milova, T., Miranda, C., Marquis, N., McMarch, M., McMan, P., Modurk, A., Macdonald, P., Marquis, N., Marphy, E., Lander, J., Milova, T., Miranda, C., Marquis, N., Marchi, C., Ollyar, T.M., Ollver, J., Miranda, C., Marquis, N., Marchi, C., Ollyar, T.M., Ollver, J., Wererson, K., Petere, N., Pisani, C., Pollara, V., Kaymond, C., Riley, R., Roove, P., Rothman, D., Stange-Thomann, W., Stojanovic, N., Subramanian, A., Tralams, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Vonner, T., Simmer, M., Marker, M., Vonner, T., Simmer, M., Marker, M., Vonner, T., Simmer, M., Marker, M., Whaman, D., Ye, W., Vonner, T., Simmer, M., Marker, M., Whaman, D., Ye, W., Vonner, T., Simmer, M., Marker, M., Wand, D., Ye, W., Vonner, T., Simmer, M., Marker, M., Wand, D., Ye, W., Vonner, T., Simmer, M., Marker, M., Wand, D., Ye, W., Vonner, T., Simmer, M., Marker, M., Wand, D., Ye, W., Wonner, T., Simmer, M., Stojanovic, M., Stoja	Direct, Submission Submitted (28 MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker. Sint, A.F.A. & Genen, P. (1996-197) Altp://itp-decome.washington.edu/RW/RepeatMasker.html Genome.washington.edu/RW/RepeatMasker.html Genome.washington.edu/RW/RepeatMasker.html Genome.washington.edu/RW/RepeatMasker.html Genome.wilk WWL site: http://www-seq.wi.mit.edu Conter ode: WIRK WWL site: http://www-seq.wi.mit.edu Gonter information Center project information Center clone name: 16875 Center clone name: 404-F_23	**NOTE: This record contains 85 individual sequencing reads that have not been assembled into contains. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-fich and allows overlap relationships among clones to be deduced. **How-ver, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will **PR # 883: qap of 100 bp p in length **PR # 883: qap of 100 bp p in length **PR # 853: contig of 882 bp in length **SA # 352: contig of 882 bp in length **SA # 353: contig of 882 bp in length **SA # 353: qap of 100 bp **SA # 354: qap of 100 bp **SA # 354: qap of 100 bp **SA # 355: qap of 100 bp **SA # 356: qap of 100
REFERENCE AUTHOR 17TEL FOTENAL FOREFERENCE AUTHORS	T L CLE J'OBRNALI GOMMENT	

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168698 bp DNA linear PRI 09-JAN-2002 AC068138.6 GI:15638958
                                                                                                                                                                                       Termination (Lases I to 141742)

Values Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA

No 63108, USA

Naterston, R.H.
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                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 41.8; DB 51.3%; Pred. No. 0.85;
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                                                                                                                                          The sequence of Homo sapiens clone Unpublished
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27382 c 25341 g 42944
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/organism="Homo sapiens
/db_xref="taxon:9606"
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Waterston, R.H.
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Best Local Similarity
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                          ORGANISM
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47432: contig of 841 bp in length
47532: gap of 100 bp
48374: contig of 842 bp in length
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  contig of 823 bp in length
                          p of 100 bp
contig of 808 bp in length
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46491: contig of 828 bp in length
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49273: contig of 799 bp in length
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61068: contig of 833 bp in length
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51.3%; Pred. No. 0.82
tive 0; Mismatches
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61169 61976: conti
61977 62076: gap of
62077 62854: conti
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44653: cont
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47432: cont
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60135: cont
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45563: con
43745:
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Best Local Similarity 51.3*
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Anote-"match to EST B1915240 (NID:d16179345)"
                                        /organism="Momo sapiens"
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      Location/Qualifiers
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6855, 6446
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9472, .9509
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17836, 17850
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7080, .7142
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18289. .18521
                                                                                    /chromosome-"2"
/map="2"
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|4327. .14408
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15177, 1505.4
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16186. 16419
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14503
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5905. .1608
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14969. 140
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                             source
      FEATURES
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Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCI. For additional information about the map position of this
sequence, see http://genome.wustl.edu/qsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Michael BAC library was made from the blood of one male donor, as described by Osegawa, K. Woon, P.Y. Zhao, E. Frengen, E. Taton, M., Catanese, J., and de Jong, P.J. (1968) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18. The clone may be obtained either from and coworkers at the Roswell Park Cancer institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The clone sequenced to the left is RPI1-314B1, 2000 bp overlap; the clone sequenced to the right is RPI1-86017. Actual start of this clone is at base position 161288 of RPI1-314B1; actual end is at
                                                                                                                                                                                                                               Direct. Submission
Submitted (28-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >> 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was contirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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unresolved di-trinucleotide repeat exists between 52436 and 52756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Water Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
Submitted (09-JAN-2002) Department of Genetics, Massouri 63108, 1
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, on Sep 18, 2001 this sequence version replaced gi:15148349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was tinished as follows unless otherwise noted:
                                                                                                    2 (bases 1 to 168698)
Isak,A., Kozlowicz,A., Doebber,A. and Dixon,R.
The sequence of Homo sapiens BAC clone RPII-813K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://wenome.wustl.edu/qsc
Contact: sapiens!watson.wustl.edu
                                           Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....Summary Statistics
Center project name: H_NHO813K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://bacpac.med.buffalo.edu)
  1 (bases 1 to 168698)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                   3 (bases 1 to 168698)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                     MC 63108, USA
5 (bases 1 to 168698)
                                                                                                                                                                                                                                                                                            My 63108, USA
4 (bases 1 to 168698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  code: WUGSC
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                                                                                                                                                                      Unpublished (2001;
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                                                                                                                                                                                                                                                                                                                                       Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
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AUTHORS
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REFERENCE
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                                           LITTE
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ALSDICONS, D.L., Manaratunge, H.C., ATE, DAIRS, J., BAIDAILA, J., BENDELONS, D.L., Manaratunge, K., Brown, E., Burch, P., Burkett, C., Burch, C., Claveland, C.D., Cox, C., Chon, E., Cox, C., Chon, E., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davis, C., Davis, C., Ding, Y., Endland, E., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Esotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Esotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Esotto, M., Falls, T., Ferraguto, D., Haves, M., Hanis, C., Harris, C., Harris, K., Hart, M., Havlak, P., Haves, M., Hanis, C., Harris, C., Hart, M., Havlak, P., Haves, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Huwes, J., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudsh, S., Karlovic, J., Lucier, R., Lucier, R., Lucier, R., Lucier, R., Lucier, R., Lucier, M., Man, J., Mapu, P., Martin, B., Martin, P., Lucier, M., Mortan, M., Mortan, P., Martin, S., Martin, C., Martin, C., Martin, C., Scherer, S., Morgan, M., Mortish, T., Warlovic, C., Martin, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shocshtari, N., Sisson, I., Sodergren, F., Primuez, E., Pull, J., Warlow, S., Savery, G., Saer, K., Tamerisa, A., Wallia, S., Wall, S., Wall, S., Wall, S., Wall, Wall, S., Wall, Wall, S., Wall, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (22-MAY-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184664)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USP.

On Nov 2, 2001 this sequence version replaced gi:16076940.

INFORMATION: http://www.ngsc.bcm.tmc.edu/ or email
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     Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANNOTATION OF FEATURES:
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Worley, K.C.
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Unpublished
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Direct Submission
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JOURNAL
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Homo sapiens 3 BAC RP11-554J1 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184664)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
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8.6%; Score 41; DB 9; Length 168698;
Best Local Similarity 61.9%; Pred. No. 1.4;
Matches 65; Conservative 0; Mismatches 40; Indels 0
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23804. 25580
23804. 25580
24583. 24621
/rpt_family="(TTTG)n"
25594. 27618
/rpt_family="L1"
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31693 .31944
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al mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
                                                                                      unpublished.) for Human and Monse sequences.
Genes and Region of Sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < le-14) to the
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flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar. and cDNA sequences. Genes demonstrate at least two exons

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

OUBLITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 19,000 bases. Reports of lowest quality individual bases and measures of base ruality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.into/qeubauk.annotarion.

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Gaps 0 Length 184564; Indels 0; Mismatches 137: Scire 47.8; DB 9: Pred. No. 1.5; 8.58; 47.68; Ouery Match Best Local Similarity 47.64 Matches 120; Conservative

DE 180886 TEGCEAGGAAGCAAFGECTAAGTFTTAAATTAAAGTAAAAATAAAGTAATCAAT 1809345 32 tagagagigiaacagicachgaictiviticaatagogagastitititicette 91

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AC026347/c Locus DEFINITION

Homo sapiens 3 BAC FP11-362A9 (FOSWOLL Lark Career Institute Human BAC Library) complete Sequence.

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Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.

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Submitted (31-OCT-2001) Human Genome Sequencing Center, Department
Submitted (31-OCT-2001) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, 77030, USA
On Oct 4, 2001 this sequence version replaced gi:15809081.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
                 STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                            unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:389-5402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                     SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .12887)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MIR"
8909. 8027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500...521
/rpt_family="AT_rich"
1223..1252
/rpt_family="AT_rich"
3700...3720
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complement(9215 9519
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10126. .10425
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complement(11240. .1
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15242. .15269
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11572. .11790
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4081. .14115
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15047. .15081
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4059. .14080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4526
ANNOTATION OF FEATURES:
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repeat_region

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

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/protein_id="Aac42363.1"
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FRORPPPOTPOTSHIFHISORRASORPEHG"
1 1183 c 1264 q 1869 t
                                                                                                            AF283102 61F2 hp 5NA linear VRF 26-LF2-2004 Xenopus laevis NKX2-5 (NKX2 5) gene, promoter region and partial
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 6152)
Sparrow Lo.B. and Mobus.1.3.
Direct Submission
Submitted (28-31N-2003) Developmental Biology NIME, The Ridgeway,
Mill Hill, London NW7 1AA, DK
                                                                                                                                                                                                                                                         Vertebrata: Buteleostomi;
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                                                                                                                                                                                                                                        Xenopus laevis
Ekkaryota: Metazota; Chordata: Craniata; Vertchrata: Buteleost.
Amphibia: Battachia; Andra; Meschattachia; Fipologa; Pipidao:
                                                                                                                                                                                                                                                                                                    Towers, N., Evans, S.M. and Mchanis, Tarink, C.B., Cooper, B., Towers, N., Evans, S.M. and Mchanis, J. Recognistion of the timman homologues in xenopus embryos 20530465
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56.4%: Pred, No. 1.8:
tive 0: Mismatches 71; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/db_xref="taxon:8455"
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1. .6152
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/qène="Nkx2-5"
/product="Nkx2-5"
5922. . »6152
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AF283102,1 GI:11991853
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1 (bases 1 to 6152)
Sparrow, D.B., Cal.C.,
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     Db 105393 TICITICAATIA 105382
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LOCUS
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VERSION
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AUTHORS
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AF106589
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KEYWORDS
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5
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complement(24430, .244coor)/rpt, family="LibK5"
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complement(24700, .24807./rpt famil
/rpt_family="AT_rich"
complement(15544, .15832)
/rpt_family="Alusx"
15833, .15856
                                                                                                                                                                                                                                                                                                                                        /rpt_family="MER7A" complement().
                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MEK§3A"
82936
                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family."MIR"
complement(23138. .23201)
/rpt_tamily="L2"
23750. .23809
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/rpt_famlly="Alusq"
complement(25458, 25541)
/rpt_famlly="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "AT_rich"
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27501, .27866
                                                           /rpt_family="AT_rich"
17828. .17850
                                                                                                                                                                                                                                                   /rpt_family-"AT_rich"
21358. .21392
/rpt_family-"AT_rich"
21637. .21659
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complement(21692..22)
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27867. 27867.
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                                                                                       17828. .17852
/rpt_family="(T)n"
17873. .18080
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20457, .20461
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complement(25550.
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18886, .18601
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76175, .26195
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23952, .23974
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24992. .2503
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.508,1022. .1195,1721. .3973,4078. .4281,5161.

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KEYWORDS

AUTHORS TITLE

REFERENCE

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

MEDLINE REFERENCE

JOURNAL

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/translation="MRAPVICRHLTYHVECQFALVTLFIVRRIEPRSIVRGDHVVHTP
LGTIRGVGQTFDGARVSAFLGVPYARPPIGSRRFKMAEMIDRWSGELEARTLAKTCYL
TIDSAPPOFPCAEMWNPPGAISEDCLNMNIWYPEDHOGSVWWYIYGGGFFSGTPSLDL
YSGSVPAARTIVVNVNYRLGFPFGYFYFDDSPIQGNMCLMDQOLALRWYHENIGAF
GGDRSRYTLFGERSGASSTTARHLFAPNSHKYRRNIINKSGSIINSMASATPPTMLDLS
FRLAKKVNCSSPDMNAIVKCLRSVPAHLVQAEADNISGDIGPPMTFAVVPVSSDANFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCSLIDFADLISDNIFGNVYMYYFTYRSSANPWPKWMCVMHGYEIEYAFGOPYMRPHL
YDQTHLEDEKRLSSIIMQIWANFANTGRTDSFWPQYNKIERKAIELGETTLQGKHRII
SDVHGGFCRMIDEAKAFVKQKNANDCRTTRKSASTEDLISSSSTTYLFSIIVYLSILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical protein Y44E3A.3"
/protein id="AAC78E30.1"
/protein id="AAC78E30.1"
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/translation="MSIAIKDDEFKTIFAEKKTOPVILFFTASWCGPCOMIKPRVEE LAAEHKDRLSILKIDVDECDGVGEEYEINSMPTFLLIVDGIKKDOFSGANNTKFEEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGDVFQKLANKQFKKDVNIIFGSVKDEGTYWLPYYMSLPKYGFAFNHTISAEDPHNRA
LITRDHYEESMRAFMPYFAGSKLVLNAFMNSYEHVSTSNVPEERYRDGVARFLGDLFF
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MPAIAPSSSALKSNFAALQERWBKILLQKKNKKNNQFPGLEFKNFKKNBLKKRNBK
WFWQKKLSEKIDSTSEFKWIPFSKRIETWNCESFSENHUSEKNOFSLFFCENFI
VLFLERMSNVLKITINLKVVAPEKVASIQKPDQRDRSSTGESTTGEPSIDNSATDOVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains similarity to thioredoxins (Pfam: PF00085, Score=99.8, E=9.3e-29, N=1)" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(17707. 17876,18825. 19047,20000. 20206,
20823. 20984,21120. 21160,21280. 21397,21513. 21677,
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                                                                                                                                                                                                                                                                                                                                               //note="C.elegans acetylcholinesterase (ACED-2)
(GB.AF025378); similar to carboxylesterases (Pfam:
PF00135, Score=363.2, E-4.9e-106, N=1); coded for by
foollowing C.elegans cDNAs: AF025378"
/codon_start=1
/product="Hotothetical protein Y44E3A.2"
/protein_id="AAC78228.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Y44E3A.3"
complement(join(15909. .16140,16338. .16429))
/gene="Y44E3A.3"
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PF00018, Score=116.8, E=4e-31, N=2); coded
following C. elegans cDNAs: yk341h3.5"
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/protein_id="AAC78229.1"
/db_xref="G1:3886087"
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/protein_id="AAC78231.1"

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    organism="Caenorhabditis elegans"

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3031. .3267,3314. .3542,3798.
/gene="Y44E3A.2"
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                                                                                                                                                                 /gene="Y44E3A.2"
/note=">---
                                                                                /db_xref="taxon:6239"
                                                 /strain="Bristol N2
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                                                                                                                                               /clone="Y44E3A"
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                                                                                                                   /chromosome="
                                                                                                                                                                                                                                   /note="ace-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
On Jun 30, 2001 this sequence version replaced gi:3886084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-JUN-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
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4444 Forest Park Avenue, St.
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Missouri 63108,
                                                                                                                                        1 (bases 1 to 48488)
The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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                                                                                                            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University, 4444 Forest Park Avenue, St. Louis, 5 (bases 1 to 48488)
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Caenorhabditis elegans
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/dothe="Y4463A.6"
/hole="contains similarity to a human autoantisen (GREDIA74), .47618,4814, .48134011,4, .48138011,5, .4825743,5, .4828573,5, .4828573,5, .4828573,5, .4828573,5, .4828573,5, .4828573,5, .4828573,5, .48286475,5, .4838511,5, .4838515,5, .4848515,5
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* 161549 166790: gap of unknown length
* 16844: contig of 1654 bp in length
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
14-JAN-2000; 2000US-0176419
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                                             specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac cell-specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac specific enhancer elements may
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                                       for
                                                                                                                                            Length 478;
                             The sequence represents the coding sequence of cardiac enh hCsx/Nkx2.5 homology domain B. The nucleic acid is useful
                                                                                                                                                               Indels
                                                                                                                Sequence 478 BP; 138 A; 129 C; 89 G; 122 T; 0 other;
                                                                                                                                           100.0%; Score 478; DB 22;
100.0%; Pred. No. 1.9e-122;
ive 0; Mismatches 0;
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           66pp; English
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                                                                                               used for gene therapy.
                                                                                                                                                                Matches 478; Conservative
                                                                                                                                                      Similarity
           Fig 5C;
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           Claim 21;
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The sequence represents the genomic sequence #2 of human Csx/Nkx2.5. The nucleic acid is useful for specifically expressing a gene in a cardiac cell, as an earlier marker of cardiomyocyte induction, e.g. for optimising cardiomyocyte induction. Genes expressed in the cardiac cell-specific manner are useful for the targeted expression of genes encoding therapeutic proteins for the treatment of damaged heart tissue. Cardiac specific enhancer elements may be used for gene therapy.
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100.0%; Pred. No. 5.1e-122;
ive 0; Mismatches 0;
(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
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Best Local Similarity 100.
Matches 478; Conservative
                                                                                                              WPI; 2001-451809/48
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                                                         Izumo S;
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Human lung antiges genomic DNA #189.

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addialerato: hepatotropic; antidiabetic; antiniflammatory; antideer; submersy; anticonvulsabt; antidiberterial; antiquals antiparasitic; cardiant; aene fherapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              celitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fundai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of genes AAC59507-C5955 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Of human servered proteins AAB34218 484264) The genes can be used to generate Inston proteins AAB34218 484264) The genes can be used to generate Inston proteins by linking to the gene for the human protein as compared to the pumen protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroidliss, diabetes mellitus, Grohn's
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Pred. No. 0.11;
0; Mismatches 34; Indels 0;
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es 62: Conservative
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P-PSDB; AAB34243.
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Luba antiqen protein; human; mouse; rabbit; quat; buse; cat; don:
chickon; sheep; immanosuperessive; artiarLuitic; vasdiropic;
artirheumatic; antiprollierative; cytostatic; cardiant; neuroproferites;
cerebioprotective; nostropic; antitactorial; vincidae; fundicide;
ophthalmological; vulnerary; que therapy; autoimmune disease; neoplasm;
                                                                               hyperproliferative disorder; breast: Hyer; cardiovascular disorder; us cerebrovascular disorder; nervous system disorder; barterial intertion; fungal intection; vorsal intection; conjar disorder; endocrine disorder; asstrointestinal disorder; respiratory disorder; sound healing; skin addie; organ transplantation; two preservative; tissue requeneration; auticinterrilly; tood admittee.
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Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode the lung antigen polypeptides of the invention. Lung antigen polypeptides of the invention. Lung antigen polypeptides and thehr associated polypucleotides are useful in the diagnosis.

Creatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular cardiovascular disorders such as cardiac arrest, cerebrovascular as cardiac arrest, cerebrovascular schemer's disease, infections caused by bacteria, viruses and fungi, cardiovascular as corneal infection, endocrine disorders such as corneal infection, to regenerate tissues and in calso be used to aid wound healing, to prevent skin aging due to sunburn, comaintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or constructive to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO cat fip., witho. int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as carebral ischaemia, nervous system disorders such as disorders such as cerebral ischaemia, nervous system disorders such as lections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, gastrointestinal disorders such as respiratory disorders such as sthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in preservative to increase or decrease storage capabilities.

Note: The sequence data for this patent did not form part of the printed section, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 362; 507pp; English.
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                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI93585 standard; cDNA; 397 BP
                                                          08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254990.
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                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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54; Conservative
                                     2000US-0251479
                                                                                                                                                                                       2001US-0259678
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                                                                                                                                                                                                                                                                          Barash SC,
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                                     06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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                                                                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA193585;
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 1; SEQ ID NO 13645; 1399pp + Sequence Listing; English.
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Best Local Similarity 56.2%; Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
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                                                                   WO200164835-A2
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPG at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 atentiurracetigatitgeaagggraatgetaatttilitetteteeagagetetea 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung antigen protein; human; mouse; rabbit; goat; horse; cat; doy;
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8.0%: Score 38.4; DB 22; Length 403;
Best Local Similarity 53.3%: Pred. No. 0.58;
Matches 81; Conservative 0; Mismatches 71; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 11490; 1399pp + Sequence Listing; English.
tissue growth factor; immunicatolistory; cancer; leukaemia; Lervous system disorders; arthritis; inflammation; ss.
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                                                                                                                                                                                                                 28-FEB-2000; 2000US-0515126.
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                                                                                                                                                                                                                                                                               (HYSE-) HYSEU INC.
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                                                                                                WC200154835-A2
                                                                                                                                                                                                                                        18-MAY-2000;
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                                                            Homo sapiens
                                                                                                                                     07-SEP-2601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders
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chicken, sheep, immunosuppressive; antiaithrith; vasciopti;
antiheumatic antipoliterative; organical crisiaar, neutroficerive;
cerebroprotective; nootropic; an idacterial; virocide; tunicide;
ophthalmological; vulnerary; agnetherapy; autoimmune disease; neglass;
hyperpoliterative disorder; bicass; liver; cacitovascular disorder; ss.
cerebroyascular disorder; nervous system disorder; bacterial intection;
quartoficestinal disorder; nervous system disorder; bacterial intection;
quartoficestinal disorder; nervous system disorder; endocrine disorder;
quartoficestinal disorder; nervous application; della disorder;
wound hadling; skin ading, organ transplantation; della preservative;
tissue regeneration; acti-intertility; tood additive.
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2000ffS-0225447.
2000ffS-0225757.
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2000US-0205515.
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2000US-0216647,
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200008 - 0225267.
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08-SEP-2000;
68-SEP-2000;
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22-AUG-2
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAS29839-AAS29930 represent cDNA molecules, which encode the lung antigen polypeptides of the invention. Lung antigen polypeptides ar their associated polynucleotides are useful in the diagnosis, treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatchd arthritis, hyperproliferative disorders such as neoplasms of the breast or liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis
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67.5%; Pred. No. 0.62;
ttive 0; Mismatches 26; Indels 0; Gaps
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                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
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06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251865.
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11-DEC-2000; 2000US-025199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptides associated with ovarian carcinomas, and the nucleuc acids that encode them, useful for the prevention diagnosis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK64788 standard; DNA; 10740 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of ovarian cancers -
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04-FEB-2000, 2000US-0180628.
24-FEB-2000, 2000US-0184664.
                                                                                                                                                                                                                              10-SEP-1999: 990S-0394374,
01-MAY-2000: 20000S-0561778
15-AUG-2000: 20000S-0640173,
U7-SEP-2000: 20000S-0656668.
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Best Local Similarity 37.2%
Technology 64: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xm J, Stolk JA;
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                                                                            15-MAR-2001.
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amino acid sequences given in AAMS1210 to AAMS1921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169 represent invention.
to AAK64702 encode the human immune/haematopoietic antigen (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 22; Length 10740; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                             Sequence 10740 BP; 3239 A; 1965 C; 2229 G; 3307 T; 0 other;
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ID AAL16112 standard; cDNA; 817
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2000US-0193480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 112; Conservative
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24-MAR-2000;
29-MAR-2000;
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AAK54951
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2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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2000US-0241786.
2000US-0241787.
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2000US-0246611.
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20-0c
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The Insention relates to Bonan Breast career expressed polynucleatides (AADS744-AALZ6789) and methods of assessing whether a patient is attlicted with breast career by examining the correlation between the expression of certain markers and the cancerous state of breast efficient progracie cides and encoded polypeptides are potential markers to. The pergracie cancer and markers and encoded polypeptides are potential markers to. For entially preventing beast cancer. The polyportides and encoded polypeptides are also useful for isolating compounds with expectative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buran; immune system disease; cytosine methylation; antiasthmatic;
antianteriosystemotics antianemis: cytoskatic; notoropic
incurporaterive; antiantifity antionomismu; ophthalmologic;
antitutammatic; antiantifity; antidiabetic; antipsoriatic;
antitutammatory; cancer eye disease; anterioscierosis; anaemia;
acute myeloid lenkamma; Azheimer's disease; Albs; epilepsy;
neurotibromatosis; rheumatoid acthritis; psoriasis; bowel disease;
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New peptide .seful as a marker for the diagnosis of breast cancer
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0; Mismarches 109; Indels o;
                                                                                                                                                                                                                                                                                                                                                                 7.9%; Seare 17.8; DB 22; Length 817;
                                                                                                                                                                                                                                                                                                  Sequence 817 EP: 182 A: 162 C; 123 G; 204 T; 147 other;
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                                       Chaim 1: Page 1550; 3695pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity 42.69
(1) Suservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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B-1.
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Matches 141: Conservative
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lex A, Fieponbrowk
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, generic analysing cytosine methylations in the pretreated DNA, generic analysing cytosine methylations in the pretreated of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV infection, neurodegenerative disorders, graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7484 TCCATTATTACGAATTTCAATTCACCAATAAATCAATAATTATTACGCACTCTACTTCCT 7425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 TCTAAATCTTCATTAAAACTACTAACCATAATACTAAATCGCTATTTCCAAAATTTAAAT 7365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                      Designing primers and probes for analysing diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or epigenetic parameters, the differences serving as basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                               cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
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Pred. No. 2.9;
0; Mismatches 107;
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ID ABL33985 standard; DNA; 11047
                                                                      2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
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Best Local Similarity 51.1%;
Matches 115; Conservative
                        15-MAR-2001; 2001WO-EP02945
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2000DE-1043826
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epillepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcorative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
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antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclarosis, anaemia; acute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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ilarity 51.1%; Pred. No. 2.9;
Conservative 0; Mismatches 107
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01-SEP-2000; 2000DE-1043826.
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nes 115; Conserv
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This sequence represents cDNA encoding human vesicular transport-related protein 11. The protein has a molecular weight of 11 kD. The invention relates to human vesicular transport-related protein 11 (AAG6666), nucleic acids encoding it (AAH7687), and a method for the recombinant production of vesicular transport-related protein 11. The present invention additionally discloses an antagonist of vesicular transport-related protein 11 for thereacutic use, and an antibody which specifically binds to vesicular transport-related protein 11 or of nucleotides which encode it may be used for treating a variety of disceases, such as malfamant unmours, blood diseases, HIV (human immunodeficiency virus) infection, immune discretes and inflammatory conditions. The protein may also be used to series and inflammatory conditions, the protein may also be used to defentification. The polynucleotide can be used as a primer for nucleic arid amplification. The polynucleotide can be used as a primer for nucleic arid amplification reactions or as a probe tor hybridisation reactions,
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                                                                                                                                                                                              /*tag= a
/product= "Human vesicular transport-related pro:ein [1"
Human; vesicular transport-related protein 11; recombinant production; mailyanat tumour; cancer; blood disease; HV infection; human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0:
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46.7%; Pred. No. 2.8;
Live 0; Mismatches 136; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                             Location/Qualitiers
4448..4756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 29-32; 36pp; Chinese.
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Bost Local Similarity 46.7
Matches 119. Conservative
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Search completed: July 5, 2002, 08:49:52 Job time: 3879 ser

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM mucleic - nucleic search, using sw model

July 5, 2002, 06:17:48; Search time 43.19 Seconds (without alignments) 2718.519 Million cell updates/sec Run on:

US-09-761-466-6 478 1 agagaaatcattacccgatt......ggcatcctccaacgacac 478 Title: Perfect score: Sequence:

383533 seqs, 122816752 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

767056

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match ()% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length	<u> </u>	ID	. Description
-	35.8	7.5	1683	4	US-39-347-803-11	Sequence 11, App)
7	35.2	7.4	2510	.7	US-18-888-982A-42	42,
m	3.5	7.3	1123	-	05-38-700-625-2	1.4
4	33.2	6.6	1129	4	US-39-227-357-40	
LC:	3.3	6.9	1059	4	US-08-163-919A-1	
Q.	3.5	6.9	1059	S	PCT-US94-14073-1	Sequence 1, Appli
7	32.8	6.9	1146	-	US-08-487-810-1	Sequence 1. Appli
æ.	32.8	6.9	1490	~	US-08-553-367A-5	LC.
Ť	32.8	6.9	1490	4	08-09-255-306-5	'n
10	32.6	6.7	176373	m	US-09-128-155-17	17,
_	32.4	6,8	1977	4	US-09-227-357-83	33
12	32.4	6.8	3300	m	US-08-913-842-4	-
~	32.4	6.8	3437	æ.	US-08-860-339-17	Sequence 17, Appl
14	31.8	6.7	9.6	৻•	US-09-248-335-57	57
15	31.6	9'9	2399	7	US-38-969-106-9	Sequence 9, Appli
16	31.4	9.9	267	2	US-08-924-838-3	
17	31.4	9.9	56516	a	US-08-996-306-1	À
18	31.4	9.6	56516	4	US-09-338-907-1	Sequence 1, Appli
5	31.4	9.9	56516	4	US-09-218-207-1	À
20	31.4	9.9	56520	4	US-09-338-907-179	Sequence 179, App
21	31.4	9.9	56520	4	US-09-218-207-179	Sequence 179, App
22	31.4	9.9	72604	4	US-09-268-952-7	Sequence 7, Appli
23	30.8	6.4	683	4	US-09-040-984-62	Sequence 62, Appl
7.4	30.8	6.4	583	₹	US-09-123-912-62	Sequence 52, Appl
25	30.8	6.4	1720	4	US-09-227-357-139	139,
26	30.8	6.4	2095	4	US-09-227-357-31	31,
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	pplicat 4379 MATION I Immodu, II Immodu, II Immodu, II Immodu, II OZCO, BB-1 OZCO, BB-1 OZTON I CATION I I ID NOS TOSOÍT (ID NOS)	al Similarity 61: Conserva? 61: Conserva? 14:49gaadaaadaadaadaagaaaaaaaaaaaaaaaaaaaaa
кимпичимимичи ОЗЭОЗЭЭОООЭЭО 8000000000000000000000000000000	RESULT 1 US-09-347-803-11 US-09-347-803-11 Sequence II Application US/09347803 GENERAL INFORMATION: APPLICANT: Famedu, Layo O. APPLICANT: Famedu, Layo O. APPLICANT: Miney. Iony APPLICANT: Kinney. Iony APPLICANT: Kinney. Iony APPLICANT: Kinney. Iony APPLICANT: Miney. Iony APPLICANT: Miney. Iony APPLICANT: Miney. Iony CURRENT FILE REFERENCE: BB-1176 CURRENT FILENG DATE: 1995-07-02 FERRIER PHILNG DATE: 1995-07-02 FERRIER FILING DATE: JOY 15, 1998 NUMHER OF SEQ ID NOS: 27 SEQ ID NO 11 LENGIH: 1683 I THE: DEGRAM OF AND	wery Match last Local Similarity fatches 61: Conserv. l46 ataggaaataaatc. l169 aaaggaaataaaaa 206 caqaactctcaaaa 206 caqaactctcaaaa 1229 caaaaaaaaaaaa cob 888 982A.42 l112 Caaaaaaaaaaaaa TILL C INVENTION. SPRICANI: BEET P TILLE OF INVENTION. NUMBER OF SPOURNES CORRESPONDENCE ADDR ADDRESSE: Jance STREET. STREET.
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APPLICATION NUMBER: 60/051,918
Diskette
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SOFTWARE: FastSEC
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MEDIUM TYPE:
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Pred. No. 0.48;
0; Mismatches 83; Indels 0
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Patent No. 5734038
Patent No. 5734038
GENERAL INFORMATION:
APPLICANT: Hillman, Janice
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                             CORRESTING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,982A
FILING DATE: Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/756,806
FILING DATE: No. 5981731ember 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07111
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250,856
FILING DATE: May 31, 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAWE: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-2401
INFORMATION FOR SEQ ID NO: 42:
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Best Local Similarity 50.6%
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STRANDEDNESS: Singl
                                                                                                                                                                   IBM 486
                                                                                                                                                                       COMPUTER: IBM 486
OPERATING SYSTEM:
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; ANTI-SENSE:
US-08-888-982A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 123 Human Secreted Proteins INTILE OF INVENTION: 123 Human Secreted Proteins CURRENT PRILING 123 Human Secreted Proteins CURRENT PILING DATE: 1999-01-08 EARLIER PILING DATE: 1999-01-07 EARLIER FILING DATE: 1998-07-07 EARLIER FILING DATE: 1997-07-08 EARLIER PILING DATE: 1997-07-08 EARLIER PILING DATE: 1997-07-08 EARLIER PILING DATE: 1997-07-08 EARLIER FILING DATE: 1997-07-08
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Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                       PF-0115 US
                                                                                            APPLICATION NUMBER: US/08/700,626
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/051,916
FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/09227357 Patent No. 6342581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1095 TGGGAAAAAAAAAAAAAAA 1117
                         YSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                              ATONICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/CDOCKET NUMBER: 9F-01
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-85-055
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLEGULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 teteaaaaaaaaaaaaaaaa 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.3%;
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.33
Best Local Similarity 63.93
Matches 53; Conservative
                                                                       CURRENT APPLICATION DATA:
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951 ATALICGAGCIGAAAACAAACAAIGAIGAIGIAAAGAAGII STINIISITIIICAAII 1810
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           GENERAL INFORMATION:
APPLICANT: THOMAS, Rayne P., CHUA, Kaw-Yah, Resers, Bruce L., and APPLICANT: KUO, Mei-chang TITLE OF INVENTION: NOSLERGE ACHES ENCODING A FORSE DEST MITE TITLE OF INVENTION: ALLERGEN, DER F-TIT, AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: THE MAS, Wayne K., CHTA, Kax-Yan. F-3EES, Frice L., and APPLICANT: KDD, Mei-chana TITLE OF INVENTION: NUCLEIC ACIDS ENVILWED BY SES JUST MITE TITLE OF INVENTION: AJLEKGEN, LEE FITL, AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.98; Score 43; 1844; Jounth 1089; Best Local Similarity 57.18; Pred. No. 1.5; Matches 50; Conservative 0; Mismatches 4*; Inde;s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TPC-072 (IMT-041)
TELEC-MANUNICATION INFORMATION:
TELEPHONE: (617) 227-7460
                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-PTWARE: ASCIL IEXT
CURRENT APPLICATION DATA:
APPLICATION NOMER: US/OF/163.519A
FILLINS DATE: 08-LEC-1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCE: 18
**O'REESPONDINTA ADDRESS:
**O'REESPONDINTA ADDRESS:
**SERET: 60 STATE STREET SOITE STA
                                                                                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Labive & Cockilold
SIREEL: 60 State Street saite 51.
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-FOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Sequence 1, Application PC/TUS9414073 : GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mandragouras, Any E.
RECISTRALION NUMBER: 34,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617) 227-7400
(517) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1059 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEU ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mai_peptide
LoCATION: 150..848
                                                                                                                                                                                                                                               Boston
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILINS DATE: 08-LEC-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53..848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US94-14073-1
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                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                         SIATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó:
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EARLIER FILING DATE: 1997-07-08
EARLIER FLILING DATE: 1997-07-08
EARLIER FLILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : NAME/KEY: SITE
: LOCATION: (1053)
: OTHER INFORMATION: n equals a,t,q, or c
US-09-227-557-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION 1997-08-18
FARLIER FILING FATE: 1997-08-18
FARLIER APPLICATION NUMBER: 60/055,964
FARLIER APPLICATION NUMBER: 60/056,360
EARLIER APPLICATION NUMBER: 60/056,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DAIE: 1997-09-12
FARLIER APPLICATION NUMBER: 60/058.661
EARLIER FILING DAIE: 1997-09-12
SUFTWARE: PATENTIN ONS: 572
SUFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60/055,684
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HARLIER FILING DATE: 1997-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAKLIER FILING DATE: 1997-08-18
EAKLIER APPLICATION NUMBER: 60/059,785
FARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1076 aaaaaaaaaaaaaaaaaaaa 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1997-08
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1997-08
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US-08-163-919A 1
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Or Gaps

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1054 AAAATCGCAGTTAAAGCATGAAACACTTGAATTGGAAAAAGAACTCTGTAGTTTGAGATT 1113
                                                                                                                                                                                                 APPLICANT: Theodor LANGE et al.

TITLE OF INVENTION: GA 20-0XIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1490;
                                                                                                                  Length 1146;
                                                                                                                                                         37; Indels
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                                                                                                                8; DB 1;
1.8;
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ilarity 59.8%; Pred. No. 2;
Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: LIBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 5939539ember 27, 1995
CLASSIFICATION: 800
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                   1114 TGCCATACAGCAAGAAAAAAAAAAAAAAAAAA 1145
                                                                                                                  Score 32.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                               203 ctccagagctctcaaaaaaaaaaaaaaaa 234
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08553367A
Patent No. 5939539
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 000
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 49/99
REFERENCE/CDCKET NUMBER: 49/97
TELECOMMUNICATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40,949
                                                                                                                  6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                  Query Match
Best Local Similarity 59.8<sup>†</sup>
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-721-8250
double
                    ; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-08-487-810-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2033 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRY: U.S.A.
20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 55; Conserv
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-553-367A-5
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                                                                                                                                                                                                                                                                               δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 6.9%; Score 33; DB 5; Length 1059; 1 Similarity 57.1%; Pred. No. 1.5; 60; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08487810

Patent No. 5618695

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: BOA ENCODING HEM-1, A GENE EXPRESSED F
TITLE OF INVENTION: SCLEROSING HEMANGIOMA CELLS

TITLE OF INVENTION: SCLEROSING HEMANGIOMA CELLS

NUMBER OF SEQUENCES: 2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,810

SEQUENCE CHARACTERISTICS:

LENGTH: 1146 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 tecagageteteaaaaaaaaaaaaaaaaaaaaaaeee 248
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: IPC-072 (IMI-041)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
TYPE: nucleic acid
                                                                      COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14073
FILING DATE: 08-DEC-1993
                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Any E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: mat_peptide
; LOCATION: 150..848
PCT-US94-14073-1
Boston
Massachusetts
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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63..848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                FILING DATE:
                                                        02109
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LOCATION:
                                     COUNTRY:
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Best Local Similarity 46.3
Matches 107; Conservative
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                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  LENGIH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-227-357-84
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                      169 tigailigeaagggcaalgetaattitititititeteeragageteteaaaaaaaaaa 228
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                                                                                                                                                                                                                               Jatell No. 5100.5.

GENERAL INFRANTION:

APPLICANT: Trecdor LANGE et al.

TITLE OF INVENTION: GA 20-0XIDASE GENE SEQUENCES (As Amended)

TITLE OF INVENTION: 19
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59.8%; Pred. No. 2;
Live 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                          SSEE: Wenderoth, Lind & Ponark, L.L.P. 2033 K Street, N.W., Suite 800 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 iach, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                1454 AAAAAAAAAAAAAAACCATGGTACCCGGAT 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/TOCKET NUMBER: 49/DIV-FD4.5MZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
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                                                                             229 aaaaaaccttactaaaaacaqqqatcccqqat 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/553,357
FILING DATE: NO. 5198021ember 27, 1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 aaaaaaccttactaaaaacagqqatcccqqat 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thallana
IMMEDIATE SGURCE:
                                                                                                                                                                                                           Sequence 5, Application US/09295305
Patent No. 5198021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1490 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskett
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Matches 55; Conservat
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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Db 106002 acaaaqaaaaaqacacaaqcttottoaaqtoataaqooyoottottaa layee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 amametgaeccaeagamitgamattmiaddaagmmmnitymemgaaaaaaaaaa 154
                                                                                                                                APPLICANT: Pain, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 PFLATED PROTEIN FAMILY
TITLE OF INVENTION: AND SSES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 100062 tuttitgeaaaaaaaatitqqaattueffeactaataetaaatiffeaffey 100112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.88; Scure 42.6; [JB 3]; 44.38; Pred; No. 16;
tive 0; Mishatches 124;
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010Pl
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EARLIER APPLICATION NUMBER: POT/USSK/) 4484
EARLIER APPLICATION NUMBER: 60/51.924
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/551.324
EARLIER APPLICATION NUMBER: 60/551.324
EARLIER APPLICATION NUMBER: 60/551.324
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/04/12P, 15A CURRENT FILING DATE: 1998-08-03
                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMER: US 60/U01, 650,
EARLIER FILING DATE: 1985-07-02
EARLIER APPLICATION NUMBER: US 60/054,647
EARLIER FILING DATE: 1937-08-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Versica.
SEQ ID NO 17
5.09-128-155-17
Sequence 17, Application US/09128155
Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : NAME/KEY: misc_leature
: LCCATION: (1)...(176473)
:/THEF INFORMATION: n = A.T.C or G
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; Patent No. 6342581
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PRAILER FILING DATE: 1997-07-08

PRAILER PILING DATE: 1997-07-08

PRAILER PILING DATE: 1997-07-08

PRAILER PILING DATE: 1997-07-08

PRAILER PLICATION NUMBER: 60/051,916

PRAILER PLICATION NUMBER: 60/051,918

PRAILER PLICATION NUMBER: 60/052,733

PRAILER PLICATION NUMBER: 60/052,733

PRAILER PLICATION NUMBER: 60/052,795

PRAILER PLICATION NUMBER: 60/052,795

PRAILER PLICATION NUMBER: 60/052,996

PRAILER PLING DATE: 1997-09-12

PRAILER PLING DATE:
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Length 1977;
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                                 Indels
                                                                                                                                                                                                                                                                                                      APPLICANT: OHBA, TOShiharu
APPLICANT: TAKARASHI, Shuichi
APPLICANT: ASAIA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: EXPRESSION USING SAID PROMOTER
TITLE OF INVENTION: EXPRESSION USING SAID PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.4; DB 3;
Pred. No. 3.5;
 DB 4;
 Score 32.4; D
Pred. No. 2.9;
                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: BROWDY AND NEIMARK, P.L.L.C. 419 7th Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 07-073043
FILING DATE: 30-MAR-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00777
FILING DATE: 26-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/913,842 FILING DATE:
                                                                                                                                                                                                                                                       Sequence 4, Application US/08913842 Patent No. 6028250
                                                                                                                                                                     1954 gggcggccgctcgcgatctaga 1975
                                                                                                                                      249 gggatcccggatgtagcctcga 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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 6.8%;
62.2%;
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TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3300 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.03
Matches 54; Conservative
                                   Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 412 ...
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US-08-913-842-4
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 Query Match
Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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US-08-913-842-4
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TITLE OF INVENTION: DNA MOLECULES CODING FOR DEBRANCHING ENZYMES DEKIVED
TITLE OF INVENTION: PROM PLANTS
FILE REFREENCE: AGREVO-6
CURRENT APPLICATION NUMBER: US/08/860.339
CURRENT FILING DATE: 1997-11-25
EARLIER APPLICATION NUMBER: DE P4447387.7
EARLIER PRILING LATE: 1994-12-22
NUMHER OF SEQ UE NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3415 geadignititgicangeataaalaaleaqiigetigitaaneataeateegataigaat 3374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 gotaattiittittitticticeagagetoteaaaaaaaaaaaaaaaaaaaaaacettactaaaaa 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
                         1471 AAAAAAAAAAAAAACTCATTTTCAAAA 1500
216 aaauzaaaaaaaaaaaaaaaaccttactaaaa 245
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/924,759
                                                                                                                                                      Sequence 17, Application US/08860339
Patent No. 6117865
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Application US/09248335
Patent No. 6096504
                                                                                                                                                                                                                                APPLICANT: Kossmann, Jens
APPLICANT: Emmermann, Michael
APPLICANT: Virgin, Ivar
APPLICANT: Renz, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Spinacia oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; [OCATION: (201)..(3095)
US-08-860-339-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6096504
GENERAL INFORMATION:
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; ORGANISM: maize
US-09-248-335-57
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                                                                                                             RESULT 13
US-08-860-339-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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ilarity 53.2%; Pred. No. 5.4;
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6.7%; Score (1.8; 14
64.0%; Pred. No. 3.2;
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APPLICANT: Vang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Scholz, V.
TITLE OF INVENTION: CDK2 INFERACITONS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: Pennie & Edmonds LLP
STREAM: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                              . Sequence 9, Application US/08969106
; Patent No. 5986055
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TELECOMMUNICALION INFORMATION:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: LOS
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APPLICATION NUMBER: US/OB
FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18.
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Search completed: July 5, 2002, 08:06:25 Job time: 6517 sec

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July 5, 2002, 06:11:43	08-09-761-466-6 478 agagaaatcattacccgatt
Pun on:	Title: Perfect score: Sequence:

[GENTITY_NOC	Gapop 10.0 , Gapext 1.0	13736207 seqs, 6748477542 residues
Scoring table:		Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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A large scale analysis of mRNAs expressed by primary mesenchyme cells of the sea urchin embryo
Development 128 (13), 2615-2627 (2001)
                                                        74 ttttttttccttccctttttgtaacacctgacccacaggactgacagttctaggaagccc 133
                                                                                                                 134 ccttacccgaaaataggaaataaatccttgccaccttgatttgcaagggcaatgctaatt 193
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/db_xref="taxon:7668"
/clone="PC_0013_A1_E11_MR"
/clone_lib="Sea urchin primary mesenchyme cell cDNA
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
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/lab_host="E.coli"
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             39;
9.5%; Score 45.6;
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Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh, P.
Tel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
Location/Qualifiers
             Pred. No.
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Drosophila melanogaster genome survey sequence T7 end of BAC BACHISTA of DrosBAC library from Drosophila melanogaster (fruit ALIO6165 arvey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                 Web: www.genoscope.ons.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryqota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pteryqota; Weoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1244)
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Letorniation of this RAZend sequence was curried out as part of a constitution of this RAZENd sequence was curried out as part of a constitution with the Borkeloy lossephila shanone brojen (Babb). The Borkeloy lossephila shanone soonstruction a physical map of the Bosophila melanousster genome using these BACS. For further information
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Erosopula melanogaster genome survey sequence 17 end of EA:
BACK24P18 of RPCI-98 library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Prosophila Genome Project (EEP) - http://www.adop.ebi.dc..his Drosophila melanomaster BAC-end European Prosophila melanomaster BAC-end Utray (Bros BA) was made by Alain Billand at CEPH (Persia d'Erder du Polymorphisme Humain) with funding provided by NEP project grant. The DNA was prefated from embryos by Alain Humain pector grant.
                                                                                  Genoscope.
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BP [9] 91006 EVEY cedex - FRANCE (E-mail : sequel genoscope cus.ir
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Contact: Walbot V
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone—end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Terraodontiformes; Terraodontidae; Tetraodon.

1 (bases 1 to 791)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J. Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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/note==_Ctp=_property | 6; Site_1: Not1; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not1 and cloned into the Not 1 and Eco RV sites of the pCMVSPGRI 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng ling Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Fmail: Lilang*lifetech.com URL:

http://tulllang*lifetech.com URL:

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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edqp.ebi.ac.uk . This Drosophila melanogaster BAC
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BP 191 91005 EVRY cedex - FRANCE (E-mail : segref/genoscope.cns.fr
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BACNISM09 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106.426.1 G1:5621382
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Pteryqota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - France
Email: segrefsqenoscope.cus.fr, Meb : www.genoscope.cns.fr.
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[J.W.H., Gruber.C., Jessee, J. and Polayes, D.
Full Hength CDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CL0BA0122G07"
/clone_lib="LTI_NFL006_PL2"
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Email: smith/email.marc.usda.acv
Single pass sequencia. Hases called act alt_rrimmed with phred
v0.980904.e. Vector identified by cross match with the eminscole 18
library (Dros BAC) was made by Alais Billand at 1988 (Centre d'Etude du Polymorphisme Humain) with jundin provided by a MRC project grant. The DNA was propared from entryss by Alain Borhoton pBelobACII.
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Mammalia; Eutheria: Cetarticdaetyla; Ruminantia; Pecora; Bovoidea;
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1. (bases 1 to 467)

Smith, 1.P.L., Grosse, W.M., Frekisa, R.A., Foint's, A.J., Stone, R.J.,
Casas, E. Wray, J.E., White, J., Che, L., Fanterkins, S.C., Bennett
G.L., Braton, M.E., Laegreid, K.W., Foilt, J.A., Chitko-McKown, C.S.
Pertea, G., Bolt, L., Karamycheva, S., Liasa, E., Quarkenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four probed-tissue normalized bovine cDNA libraries and construction of a deno index for calle Genome Res. II (4), 625-630 (20\%) 21180013
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49.0%: Pred. No. 2.7e-92:
ative 19; Mismarches 44; Indexs 0;
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B15408421 G1:15:81954
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    /ordanism "Drosophila melanogastes"
    /ptasmid-"pReloMACII"

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Po Box 165, Clay Center, NE (Reversible, USA
Tel: 402-762-4366
Fax: 402-762-4399
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/rlone_lib-"Makk; 18 vv"

/tissue_lype "fooled"

/lab_host "EHIUP"
                                                                                                                                                                                                                        /db_xret-"(axon:222"
/clone_lib-"proshAN"
/clone-"BACN35Moy"
/note-"end : SFF"
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L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutczyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: nbw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNSOO4YY

CNSOO4YY

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACRIF03 of RPCI-98 library from Drosophila melanogaster (fruit
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/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Librairy made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                        cacctgacccacaggactgacagttctaggaagccccttacccgaaaataggaaataaa 157
                                                                                                                                                                                                                                                                                              fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                                                                   8.5%; Score 40.6; DB 10;
llarity 54.3%; Pred. No. 5.7e+02;
Conservative 0; Mismatches 69;
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16.4%; Pred. No. 4.2e+02;
Live 85; Mismatches 53;
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this PAC-end sequence was carried out as part of a collaboration with the Berkeley prosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS00GQG 980 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR33J07 of RPCI-98 library from Drosophila melanogaster (fruit
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                     693 ЖНҮНҮҮНҮҮҮҮҮНҮААРАҮҮНӨУҮҮҮАҮНҮҮҮҮАГӨНӨНӨНӨНӨӨҮӨҮҮҮҮҮНҮӨАӨААР 752
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/db_xref="taxon:7227"
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9.2%; Pred. No. 3.9e+02;
ve 56; Mismatches 65;
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Best Local Similarity 29.2%; Pro
Matches 50; Conservative 56;
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                                                                                                                                                                                                                                              CNS05677R 11near GSS 26-MAY-2000 Tetracodon nigroviridis genome survey sequence 13 end of clone 023A68 of library A from Tetracodon nigroviridis, genomic survey
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Actinopteryqii, Neopteryqii, Teleostei, Buteleostei, Neoteleostei,
Acantlomorpha, Acanthopteryqii, Percomorpha, Tetraodontiformes,
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(buses 1 to 385)
Roses-Trollius, H., Jaillou, F., Dasilva, C., Firames, C., Fisher, C., Roser-Trollius, H., Jaillou, F., Outrier, F., Saurin, W., Nermet, A., and Weissenbach, J.
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/dr.aree-"taxon:99883"
/clone-1023A08"
/clone-lib-Arabes sequence ID : CGAAU238AU4Al-end : 13"
1 211 c 122 q 201 t, 168 others
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Best Local Similarity 54.5%; Pred. No. 3.9e-02;
Matches 60; Conservative 0; Mismatches 50; Indeis 0;
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Tetracdon nigroviridis.
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